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Jiangchun Xu

Title

**COMPOUNDS FOR IMMUNODIAGNOSIS OF  
PROSTATE CANCER AND METHODS FOR  
THEIR USE**

(Only for nonprovisional applications under 37 CFR § 1.53(b))

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**APPLICATION ELEMENTS**

See MPEP chapter 600 concerning utility patent application contents.

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1. <input checked="" type="checkbox"/> General Authorization Form (Submit an original and a duplicate for fee processing)	6. <input type="checkbox"/> Microfiche Computer Program (Appendix)	
2. <input checked="" type="checkbox"/> Specification [Total Pages] (preferred arrangement set forth below)	134	7. <input type="checkbox"/> Nucleotide and Amino Acid Sequence Submission (if applicable, all necessary)
<ul style="list-style-type: none"> <li>- Descriptive Title of the Invention</li> <li>- Cross References to Related Applications</li> <li>- Statement Regarding Fed sponsored R &amp; D</li> <li>- Reference to Microfiche Appendix</li> <li>- Background of the Invention</li> <li>- Brief Summary of the Invention</li> <li>- Brief Description of the Drawings (if filed)</li> <li>- Detailed Description</li> <li>- Claim(s)</li> <li>- Abstract of the Disclosure</li> </ul>		
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Continuation  Divisional  Continuation-In-Part (CIP) of prior Application No.: Not Available

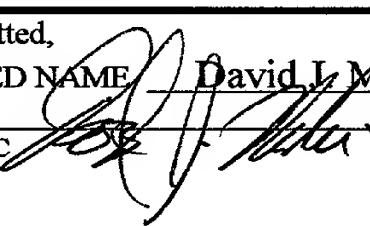
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COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER  
AND METHODS FOR THEIR USE

REFERENCE TO RELATED APPLICATIONS

5                   This application is a continuation-in-part of U.S. Patent Application No. \_\_\_\_\_, filed February 9, 1998 (Attorney Docket No. 210121.428C2), which is a continuation-in-part of U.S. Patent Application No. 08/904,809, filed August 1, 1997, which is a continuation-in-part of U.S. Patent Application No. 08/806,596, filed February 25, 1997.

10

TECHNICAL FIELD

15                   The present invention relates generally to the treatment and monitoring of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein. Such polypeptides may be used for the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of prostate cancer, and possibly other tumor types, in a patient.

BACKGROUND OF THE INVENTION

20                   Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

25                   In spite of considerable research into diagnosis and therapy of the disease, prostate cancer remains difficult to detect and to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited 30 diagnostic and therapeutic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA

measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved and diagnostic methods for prostate cancer.

5

## SUMMARY OF THE INVENTION

The present invention provides methods for immunodiagnosis of prostate cancer, together with kits for use in such methods. Polypeptides are disclosed which comprise at least an immunogenic portion of a prostate tumor protein or a variant of 10 said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224 and 15 variants thereof. Such polypeptides may be usefully employed in the diagnosis and monitoring of prostate cancer.

In one specific aspect of the present invention, methods are provided for detecting prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; and (b) detecting in the sample a protein or polypeptide that binds 20 to the binding agent. In preferred embodiments, the binding agent is an antibody, most preferably a monoclonal antibody.

In related aspects, methods are provided for monitoring the progression of prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above 25 polypeptides; (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent; (c) repeating steps (a) and (b); and comparing the amounts of polypeptide detected in steps (b) and (c).

Within related aspects, the present invention provides antibodies, preferably monoclonal antibodies, that bind to the inventive polypeptides, as well as 30 diagnostic kits comprising such antibodies, and methods of using such antibodies to inhibit the development of prostate cancer.

The present invention further provides methods for detecting prostate cancer comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with a first and a second oligonucleotide primer in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers. In a preferred embodiment, at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In a further aspect, the present invention provides a method for detecting prostate cancer in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe. Preferably, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In related aspects, diagnostic kits comprising the above oligonucleotide probes or primers are provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

25

#### DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunodiagnosis and monitoring of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant thereof such a protein, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences 5 recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist 10 entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted 15 with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for 20 example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I- 25 labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as 30 used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants

preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of one of the above polypeptides, and evaluating 5 the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

10 As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, 15 asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

20 Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs 25 transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

30 A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and

most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recite nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; 5 followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate 10 tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA 15 molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID Nos: 1-107, 20 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence 25 encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 30 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase

techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems 5 Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of 10 expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells 15 employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are 20 homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods 25 disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker 30 peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA

sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA 5 translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into 10 the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide 15 functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent 20 No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable 25 transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

30 Polypeptides and/or fusion proteins of the present invention may be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention

may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide and/or fusion protein prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides and/or fusion proteins capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate

cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of one or more of the above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include 5 blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent 10 association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant 15 is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

20 Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. 25 Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 30 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second

binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the 5 binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be 10 a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support 15 using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). 20 Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or 25 polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10  $\mu$ g, and preferably about 100 ng to about 1  $\mu$ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with 30 both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an

aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay.

5 This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a

10 different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically

15 blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20<sup>TM</sup> (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact

20 time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve

25 equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20<sup>TM</sup>. The second

30 antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and

biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide.

5 An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate.

10 Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction

15 products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the

20 immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for*

25 *Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the

30 most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or

to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or 5 strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody 10 may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area 15 of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in 20 the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use 25 with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the 30 level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of

polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding

activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the 5 yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process 10 in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation 15 inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include <sup>90</sup>Y, <sup>123</sup>I, <sup>125</sup>I, <sup>131</sup>I, <sup>186</sup>Re, <sup>188</sup>Re, <sup>211</sup>At, and <sup>212</sup>Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

20 A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group 25 containing a good leaving group (*e.g.*, a halide) on the other.

30 Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in

chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described 5 in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulphydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody 10 portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a 15 photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one 20 embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for 25 attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may 30 also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating

compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For 5 example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the 10 precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a 15 polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a 20 DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, 25 preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected 30 from SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided

in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis et al. *Ibid*; Ehrlich, *Ibid*). Primers or probes may thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, 5 prostate tissue and/or prostate tumor tissue.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may also be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for 10 using one or more of the immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NO: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. 15 Accordingly, the above immunoreactive polypeptides may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide is generally present within a 20 pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (*e.g.*, polylactic 25 galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (*i.e.*, a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain 30 DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in

the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (i.e., untreated) level. In

general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1  $\mu$ g. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to 5 about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a 10 lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable 15 microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of 20 immune response, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment 25 of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE<sup>TM</sup> system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of 30 the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-

specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

The following Examples are offered by way of illustration and not by  
5 way of limitation.

## EXAMPLES

### EXAMPLE 1

#### 10 ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from  
15 prostate tumor poly A<sup>+</sup> RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A<sup>+</sup> RNA  
20 was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns  
25 (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA  
30 libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64 x 10<sup>7</sup> independent colonies, with 70% of

clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained  $3.3 \times 10^6$  independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence 5 and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara et al. (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted 10 cDNA library was generated as follows. Normal pancreas cDNA library (70  $\mu$ g) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100  $\mu$ l of H<sub>2</sub>O, heat-denatured and mixed with 100  $\mu$ l (100  $\mu$ g) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As 15 recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50  $\mu$ l) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23  $\mu$ l H<sub>2</sub>O to form the driver DNA.

To form the tracer DNA, 10  $\mu$ g prostate tumor cDNA library was 20 digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5  $\mu$ l H<sub>2</sub>O. Tracer DNA was mixed with 15  $\mu$ l driver DNA and 20  $\mu$ l of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The 25 sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12  $\mu$ l H<sub>2</sub>O, mixed with 8  $\mu$ l driver DNA and 20  $\mu$ l of 2 x hybridization buffer, and subjected to a hybridization at 68 30 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol

resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library(prostate subtraction 1.

To analyze the subtracted cDNA library, plasmid DNA was prepared  
5 from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be  
10 abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID No: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known  
15 sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously  
20 identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

25 To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1  $\mu$ g each of human glandular kallikrein, PSA and  
30 mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second

subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for 5 the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-63, L1-4 and L1-14 are provided in SEQ ID Nos: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, 10 N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID Nos: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID Nos: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to 15 be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID Nos:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 20 and N1-1860; SEQ ID Nos: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID Nos: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID Nos: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 25 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by 30 subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-

3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was 5 performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-10 3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and 15 prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described 20 above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 25 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 30 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated

clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

5 Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described  
10 above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

15 cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a  
20 unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-  
25 expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences  
30 with those in the gene bank as described above, revealed some homology to previously identified ESTs.

## EXAMPLE 2

## DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

5

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2  $\mu$ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42  $^{\circ}$ C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR,  $\beta$ -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using  $\beta$ -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the  $\beta$ -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the  $\beta$ -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17

and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR 5 results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, 10 detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

15 Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the 20 other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

25 The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected 30 in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal

prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

### Example 3

#### 10 ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, 15 placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was 20 isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, 25 P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79, and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of 30 these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were

found to show no significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to 5 previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences 10 being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, 15 kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate 20 tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was 25 found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For 30 P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal

PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) 5 compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of sixteen additional clones. The determined DNA sequences for these clones are provided in SEQ ID NO: 207-222.

10

#### EXAMPLE 4

#### SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on an Applied Biosystems 430A 15 peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: 20 trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to 25 elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific 30 embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANTS: Xu, Jiangchun  
Dillon, Davin C.

(ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER  
AND METHODS FOR THEIR USE

(iii) NUMBER OF SEQUENCES: 224

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(D) STATE: WA  
(E) COUNTRY: USA  
(F) ZIP: 98104

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 23-FEB-1998  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.  
(B) REGISTRATION NUMBER: 31,392  
(C) REFERENCE/DOCKET NUMBER: 210121.428C3

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 622-4900  
(B) TELEFAX: (206) 682-6031

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TTTTCACAG TATAACAGCT CTTTATTCT GTGAGTTCTA CTAGGAAATC	60
ATCAAATCTG AGGGTTGTCT GGAGGGACTTC AATACACCTC CCCCCATAGT GAATCAGCTT	120
CCAGGGGGTC CAGTCCCTCT CCTTACTTCA TCCCCATCCC ATGCCAAAGG AAGACCCTCC	180
CTCCTTGGCT CACAGCCTTC TCTAGGCTTC CCAGTGCCTC CAGGACAGAG TGGGTTATGT	240

TTTCAGCTCC	ATCCTTGCTG	TGAGTGTCTG	GTGCGTTGTG	CCTCCAGCTT	CTGCTCAGTG	300
CTTCATGGAC	AGTGTCCAGC	ACATGTCACT	CTCCACTCTC	TCAGTGTGGA	TCCACTAGTT	360
CTAGAGCGGC	CGCCACCGCG	GTGGAGCTCC	AGCTTTGTT	CCCTTAGTG	AGGGTTAATT	420
GCGCGCTTGG	CGTAATCATG	GTCATAACTG	TTTCCTGTGT	GAAATTGTTA	TCCGCTCACA	480
ATTCCACACA	ACATACGAGC	CGGAAGCATA	AAGTGTAAAG	CCTGGGGTGC	CTAATGAGTG	540
ANCTAACTCA	CATTAATTGC	GTTGCGCTCA	CTGNCCGCTT	TCCAGTCNGG	AAAACGTGCG	600
TGCCAGCTGC	ATTAATGAAT	CGGCCAACGC	NCGGGGAAAA	GCGGTTTGC	TTTGGGGGC	660
TCTTCCGCTT	CTCGCTCACT	NANTCCTGCG	CTCGGTCNTT	CGGCTGCAGG	GAACGGTATC	720
ACTCCTCAAA	GGNGGTATTA	CGGTTATCCN	NAAATCNGG	GATACCCNGG	AAAAAANTTT	780
					AACAAAAGGG	CANCAAAGGG
					CNGAAACGTA	AAAA

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACAGAAATGT	TGGATGGTGG	AGCACCTTTC	TATACGACTT	ACAGGACAGC	AGATGGGGAA	60
TTCATGGCTG	TTGGAGCAAT	AGAACCCAG	TTCTACGAGC	TGCTGATCAA	AGGACTTGGA	120
CTAAAGTCTG	ATGAACCTCC	CAATCAGATG	AGCATGGATG	ATTGGCCAGA	AATGAAGAAG	180
AAGTTTGCAG	ATGTATTTGC	AAAGAAGACG	AAGGCAGAGT	GGTGTCAAAT	CTTGACGGC	240
ACAGATGCCT	GTGTGACTCC	GGTTCTGACT	TTTGAGGAGG	TTGTTCATCA	TGATCACAAC	300
AAGGAACGGG	GCTCGTTAT	CACCAAGTGA	GAGCAGGACG	TGAGCCCCCG	CCCTGCACCT	360
CTGCTGTTAA	ACACCCAGC	CATCCCTTCT	TTCAAAAGGG	ATCCACTAGT	TCTAGAACGCG	420
GCCGCCACCG	CGGTGGAGCT	CCAGCTTTG	TTCCCTTTAG	TGAGGGTTAA	TTGCGCGCTT	480
GGCGTAATCA	TGGTCATAGC	TGTTCTGT	GTGAAATTGT	TATCCGCTCA	CAATTCCCCC	540
AACATACGAG	CCGGAACATA	AAAGTGTAAAG	CCTGGGGTGC	CTAATGANTG	AGCTAACTCN	600
CATTAATTGC	GTTGCGCTCA	CTGCCGCTT	TCCAGTCAGG	AAAACGTGCG	TGCCACTGCN	660
TTANTGAATC	NGCCACCCCC	CGGGAAAAGG	CGGTTGCNTT	TTGGGCCTCT	TCCGCTTTCC	720
TCGCTCATTG	ATCCTNGCNC	CCGGTCTTCG	GCTGCGGNGA	ACGGTTCACT	CCTCAAAGGC	780
GGTNTNCCGG	TTATCCCCAA	ACNGGGATA	CCCNGA			816

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTTTGAAAG	AAGGGATGGC	TGGGGTGT	AACAGCAGAG	GTGCAGGGCG	GGGGCTCACG	60
TCCTGCTCCT	CACTGGTGAT	AAACGAGCCC	CGTTCTTGT	TGTGATCATG	ATGAACAAACC	120
TCCTCAAAAG	TCAGAACCGG	AGTCACACAG	GCATCTGTGC	CGTCAAAGAT	TTGACACCAC	180
TCTGCCTTCG	TCTTCTTGC	AAATACATCT	GCAAACCTCT	TCTTCATTTC	TGGCCAATCA	240
TCCATGCTCA	TCTGATTGGG	AAGTCATCA	GACTTAGTC	CANNTCTTT	GATCAGCAGC	300
TCGTAGAACT	GGGGTTCTAT	TGCTCCAACA	GCCATGAATT	CCCCATCTGC	TGTCCTGTAA	360
GTCGTATAGA	AAGGTGCTCC	ACCATCCAAC	ATGTTCTGTC	CTCGAGGGGG	GGCCCGGTAC	420
CCAATTGCGC	CTATANTGAG	TCGTATTACG	CGCGCTCACT	GGCCGTCGTT	TTACAACGTC	480

GTGACTGGGA AAACCCTGGG CGTTACCAAC TTAATGCCT TGAGCACAT CCCCCTTTCG	540
CCAGCTGGC GTAATANGA AAAGGCCGC ACCGATGCC CTTCCAACAG TTGCGCACCT	600
GAATGGGNAATGGGACCCC CCTGTTACCG CGCATTNAAC CCCCNGGG TTTNGTTGTT	660
ACCCCCACNT NNACCGCTTA CACTTGCCA GCGCCTTANC GCCCGCTCCC TTTCNCCTT	720
CTTCCCTTCC TTTCNCNCN CTTCCCCCG GGGTTTCCCC CNTCAAACCC CNA	773

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCCTGAGT CCTACTGACC TGTGCTTCT GGTGTGGAGT CCAGGGCTGC TAGGAAAAGG	60
AATGGGCAGA CACAGGTGTA TGCCAATGTT TCTGAAATGG GTATAATTTC GTCCTCTCCT	120
TCGGAACACT GGCTGTCTCT GAAGACTTCT CGCTCAGTT CAGTGAGGAC ACACACAAAG	180
ACGTGGGTGA CCATGTTGTT TGTGGGGTGC AGAGATGGGA GGGGTGGGGC CCACCCTGGA	240
AGAGTGGACA GTGACACAAG GTGGACACTC TCTACAGATC ACTGAGGATA AGCTGGAGCC	300
ACAATGCATG AGGCACACAC ACAGCAAGGA TGACNCTGTA AACATAGCCC ACGCTGTCT	360
GNGGGCAGTG GGAAGCCTAN ATNAGGCCGT GAGCANAAG AAGGGGAGGA TCCACTAGTT	420
CTANAGCGGC CGCCACCGCG GTGGANCTCC ANCTTTGTT CCCTTAGTG AGGGTTAATT	480
GCGCGCTTGG CNTAATCATG GTCATANCTN TTTCTGTGT GAAATTGTTA TCCGCTCACAA	540
ATTCCACACA ACATACGANC CGGAAACATA AANTGTAAAC CTGGGGTGCC TAATGANTGA	600
CTAACTCACA TTAATTGCGT TGCGCTCACT GCCCGCTTC CAATCNGGAA ACCTGTCTTG	660
CCNCTTGCAT TNATGAATCN GCCAACCCCC GGGAAAAGC GTTGCCTT TGGCGCTCT	720
TCCGCTTCCT CNCTCANTTA NTCCCTNCNC TCGGTCAATT CGGCTGCNGC AAACCGGTTCA	780
ACCNCTCCA AAGGGGTAT TCCGGTTCC CCNAATCCGG GGANANCC	828

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTTT TTTTTACTGA TAGATGGAAT TTATTAAGCT TTTCACATGT GATAGCACAT	60
AGTTTTAATT GCATCCAAAG TACTAACAAA AACTCTAGCA ATCAAGAATG GCAGCATGTT	120
ATTTTATAAC AATCAACACC TGTGGCTTT AAAATTGTT TTTCATAAGA TAATTTATAC	180
TGAAGTAAAT CTAGCCATGC TTTTAAAAAA TGCTTAGGT CACTCCAAGC TTGGCAGTTA	240
ACATTGGCA TAAACAATAA TAAAACAATC ACAATTAAAT AAATAACAAA TACAACATTG	300
TAGGCCATAA TCATATACAG TATAAGGAAA AGGTGGTAGT GTTGAGTAAG CAGTTATTAG	360
AATAGAATAC CTTGGCCTCT ATGCAAATAT GTCTAGACAC TTTGATTCA TCAGCCCTGA	420
CATTCAGTT TCAAAGTAGG AGACAGGTTCA TACAGTATCA TTTTACAGTT TCCAACACAT	480
TGAAAACAAG TAGAAAATGA TGAGTTGATT TTTATTAATG CATTACATCC TCAAGAGTTA	540
TCACCAACCC CTCAGTTATA AAAAATTTC AAGTTATATT AGTCATATAA CTTGGTGTGC	600
TTATTTAAA TTAGTGCTAA ATGGATTAAG TGAAGACAAAC AATGGTCCCC TAATGTGATT	660
GATATTGGTC ATTTTACCA GCTTCTAAAT CTNAACTTTC AGGCTTTGA ACTGGAACAT	720
TGNATNACAG TGTTCCANAG TTNCAACCTA CTGGAACATT ACAGTGTGCT TGATTCAAAA	780

TGTTATTTG TTAAAAATTA AATTTAACCC TGGTGGAAAA ATAATTTGAA ATNA 834

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTT	TTTTTTTTT	AAGACCCTCA	TCAATAGATG	GAGACATACA	GAAATAGTCA	60
AACCACATCT	ACAAAATGCC	AGTATCAGGC	GGCGGCTTCG	AAGCCAAAGT	GATGTTGGA	120
TGTAAAGTGA	AATATTAGTT	GGCGGATGAA	GCAGATAGTG	AGGAAAGTTG	AGCCAATAAT	180
GACGTGAAGT	CCGTGGAAGC	CTGTGGCTAC	AAAAAATGTT	GAGCCGTAGA	TGCCGTGGA	240
AATGGTGAAG	GGAGACTCGA	AGTACTCTGA	GGCTTGTAGG	AGGGTAAAAT	AGAGACCCAG	300
TAAAATTGTA	ATAAGCAGTG	CTTGAATTAT	TTGGTTTCGG	TTGTTTCTA	TTAGACTATG	360
GTGAGCTCAG	GTGATTGATA	CTCCTGATGC	GAGTAATACG	GATGTGTTA	GGAGTGGGAC	420
TTCTAGGGGA	TTTAGCGGGG	TGATGCCTGT	TGGGGGCCAG	TGCCCTCCTA	GTTGGGGGGT	480
AGGGGCTAGG	CTGGAGTGGT	AAAAGGCTCA	GAAAAATCCT	GCGAAGAAAA	AAACTTCTGA	540
GGTAATAAT	AGGATTATCC	CGTATCGAAG	GCCTTTTGG	ACAGGTGGTG	TGTGGTGGCC	600
TTGGTATGTG	CTTCTCGTG	TTACATCGCG	CCATCATTGG	TATATGGTTA	GTGTGTTGGG	660
TTANTANGGC	CTANTATGAA	GAACCTTTGG	ANTGGAATT	AATCAATNGC	TTGGCCGGAA	720
GTCATTANGA	NGGCTNAAA	GGCCCTGTTA	NGGGTCTGGG	CTNGGTTTA	CCCNACCCAT	780
GGAATNCNCC	CCCCGGACNA	NTGNATCCCT	ATTCTTAA			818

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTT	TTTTTTTTT	TGGCTCTAGA	GGGGTAGAG	GGGGTGTAT	AGGGTAAATA	60
CGGGCCCTAT	TTCAAAGATT	TTTAGGGAA	TTAATTCTAG	GACGATGGGT	ATGAAACTGT	120
GGTTTGCTCC	ACAGATTCA	GAGCATTGAC	CGTAGTATAC	CCCCGGTCGT	GTAGCGGTGA	180
AAGTGGTTG	GTTCAGACGT	CCGGGAATTG	CATCTGTTT	TAAGCCTAAT	GTGGGGACAG	240
CTCATGAGTG	CAAGACGTCT	TGTGATGTA	TTATTATACN	AATGGGGCT	TCAATCGGGA	300
GTACTACTCG	ATTGTCAACG	TCAAGGAGTC	GCAGGTGCGC	TGGTTCTAGG	AATAATGGGG	360
GAAGTATGTA	GGAATTGAAG	ATTAATCCGC	CGTAGTCGGT	GTTCTCCTAG	GTTCAATACC	420
ATTGGTGGCC	AATTGATTTG	ATGGTAAGGG	GAGGGATCGT	TGAACTCGTC	TGTTATGTAA	480
AGGATNCCTT	NGGGATGGGA	AGGCNATNAA	GGACTANGGA	TNAATGGCGG	GCANGATATT	540
TCAAACNGTC	TCTANTCCT	GAAACGTCTG	AAATGTTAAT	AANAATTAAN	TTTNGTTATT	600
GAATNTTNNG	GAAAAGGGCT	TACAGGACTA	GAAACCAAAT	ANGAAAANTA	ATNNTAANGG	660
CNTTATCNTN	AAAGGTNATA	ACCNCTCCTA	TNATCCCACC	CAATNGNATT	CCCCACNCNN	720
ACNATTGGAT	NCCCCANTTC	CANAAANGGC	CNCCCCCGG	TGNANNCCNC	CTTTGTTCC	780
CTTNANTGAN	GGTTATTCNC	CCCTNGCNTT	ATCANCC			817

(2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTTCCGGG	TTTACTTTCT	AAGGAAAGCC	GAGCGGAAGC	TGCTAACGTG	GGAATCGGTG	60
CATAAGGAGA	ACTTTCTGCT	GGCACGCGCT	AGGGACAAGC	GGGAGAGCGA	CTCCGAGCGT	120
CTGAAGCGCA	CGTCCCAGAA	GGTGGACTTG	GCACTGAAAC	AGCTGGGACA	CATCCGCGAG	180
TACGAACAGC	GCCTGAAAGT	GCTGGAGCGG	GAGGTCCAGC	AGTGTAGCCG	CGTCCTGGGG	240
TGGGTGGCCG	ANGCTGANC	CGCTCTGCCT	TGCTGCCCCC	ANGTGGGCCG	CCACCCCCCTG	300
ACCTGCCTGG	GTCCAAACAC	TGAGCCCTGC	TGGCGGACTT	CAAGGANAAC	CCCCACANGG	360
GGATTTGCT	CCTANANTAA	GGCTCATCTG	GGCCTCGGCC	CCCCCACCTG	GTTGGCCTTG	420
TCTTGANGT	GAGCCCCATG	TCCATCTGGG	CCACTGTCTG	GACCACCTT	NGGGAGTGT	480
CTCCTTACAA	CCACANNATG	CCCGGCTCCT	CCCGGAAACC	ANTCCCANCC	TGNGAAGGAT	540
CAAGNCCTGN	ATCCACTNNT	NCTANAACCG	GCCNCCNCCG	CNGTGGAAC	CNCCTTNTGT	600
TCCTTTTCNT	TNAGGGTTAA	TNNCGCCTTG	GCCTTNCCAN	NGTCCTNCNC	NTTTTCCNN	660
GTTNAAATTG	TTANGCNCCC	NCCNNTCCCN	CNNCNNCNAN	CCCGACCCNN	ANNTTNNANN	720
NCCTGGGGGT	NCCNINCNGAT	TGACCCNNCC	NCCCTNTANT	TGCNTTNGGG	NNCNNTGCC	780
CTTCCCTCT	NGGGANNCG					799

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCCTTGAT	CCTCCCAGGC	TGGGACTGGT	TCTGGGAGGA	GCCGGGCATG	CTGTGGTTG	60
TAANGATGAC	ACTCCCAAAG	GTGGTCCTGA	CAGTGGCCA	GATGGACATG	GGGCTCACCT	120
CAAGGACAAG	GCCACCAGGT	GCGGGGGCCG	AAGCCCACAT	GATCCTTACT	CTATGAGCAA	180
AATCCCCTGT	GGGGGCTTCT	CCTTGAAGTC	CGCCANCAGG	GCTCAGTCTT	TGGACCCANG	240
CAGGTTCATGG	GGTTGTNGNC	CAACTGGGGG	CCNCAACGCA	AAANGCNCA	GGGCCTCNGN	300
CACCCATCCC	ANGACGCGGC	TACACTNCTG	GACCTCCNC	TCCACCAC	TCATGCGCTG	360
TTCNTACCCG	CGNATNTGTC	CCANCTGTT	CNGTGCCNAC	TCCANCTTCT	NGGACGTGCG	420
CTACATACGC	CCGGANTCNC	NCTCCCGCTT	TGTCCCTATC	CACGTNCCAN	CAACAAATT	480
CNCCNTANTG	CACCNATTCC	CACNTTNC	AGNTTCCNC	NNCGNGCTTC	CTTNTAAAAG	540
GGTTGANCCC	CGGAAAATNC	CCCAAAGGGG	GGGGGCCNGG	TACCCAACTN	CCCCCTNATA	600
GCTGAANTCC	CCATNACCNN	GNCTCNATGG	ANCCNTCCNT	TTAANNACN	TTCTNAACTT	660
GGGAANANCC	CTCGNCCNTN	CCCCNNTAA	TCCCNCTTG	CNANGNNCNT	CCCCCNNTCC	720
NCCCNNTNG	GCNTNTNANN	CNAAAAGGC	CCNNNANCAA	TCTCCTNNCN	CCTCANTTCG	780
CCANCCCTCG	AAATCGGCCN	C				801

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGTCTATNT	GGCCAGTGTG	GCAGCTTC	CTGTGGCTGC	CGGTGCCACA	TGCCTGTCCC	60
ACAGTGTGGC	CGTGGTGACA	GCTTCAGCCG	CCCTCACCGG	GTTCACCTTC	TCAGCCCTGC	120
AGATCCTGCC	CTACACACTG	GCCTCCCTCT	ACCACCGGGA	GAAGCAGGTG	TTCCCTGCCA	180
AATAACCGAGG	GGACACTGGA	GGTGCTAGCA	GTGAGGACAG	CCTGATGACC	AGCTTCCTGC	240
CAGGCCCTAA	GCCTGGAGCT	CCCTTCCCTA	ATGGACACGT	GGGTGCTGGA	GGCAGTGGCC	300
TGCTCCCACC	TCCACCCGCG	CTCTGCGGGG	CCTCTGCCTG	TGATGTCTCC	GTACGTGTGG	360
TGGTGGGTGA	GCCCACCGAN	GCCAGGGTGG	TTCCGGGCCG	GGGCATCTGC	CTGGACCTCG	420
CCATCCTGGA	TAGTGCTTC	TGCTGTCCCA	NGTGGCCCCA	TCCCTGTTA	TGGGCTCCAT	480
TGTCCAGCTC	AGCCAGTCTG	TCACTGCCTA	TATGGTGTCT	GCCGCAGGCC	TGGGTCTGGT	540
CCCATTTACT	TTGCTACACA	GGTANTATT	GACAAGAACG	ANTTGGCCAA	ATACTCAGCG	600
TTAAAAAAATT	CCAGCAACAT	TGGGGGTGGA	AGGCCTGCCT	CACTGGGTCC	AACTCCCCGC	660
TCCTGTTAAC	CCCATGGGGC	TGCCGGCTTG	GCCGCCAATT	TCTGTTGCTG	CCAAANTNAT	720
GTGGCTCTCT	GCTGCCACCT	GTTGCTGGCT	GAAGTGCNTA	CNGNCANCT	NGGGGGGTNG	780
					GGNGTTCCC	789

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCACCCCTAC	CCAAATATTA	GACACCAACA	CAGAAAAGCT	AGCAATGGAT	TCCCTTCTAC	60
TTTGTAAAT	AAATAAGTTA	AATATTTAAA	TGCCTGTGTC	TCTGTGATGG	CAACAGAAAGG	120
ACCAACAGGC	CACATCCTGA	TAAAAGGTAA	GAGGGGGGTG	GATCAGCAAA	AAGACAGTGC	180
TGTGGGCTGA	GGGGACCTGG	TTCTTGTGTG	TTGCCCTCA	GGACTCTTCC	CCTACAAATA	240
ACTTCATAT	GTTCAAATCC	CATGGAGGAG	TGTTTCATCC	TAGAAACTCC	CATGCAAGAG	300
CTACATTAAA	CGAAGCTGCA	GGTTAAGGGG	CTTANAGATG	GGAAACCAGG	TGACTGAGTT	360
TATTCAGCTC	CCAAAAAACCC	TTCTCTAGGT	GTGTCTCAAC	TAGGAGGCTA	GCTGTTAACCC	420
CTGAGCCTGG	GTAATCCACC	TGCAGAGTCC	CCGCATTCCA	GTGCATGGAA	CCCTTCTGGC	480
CTCCCTGTAT	AAGTCCAGAC	TGAAACCCCC	TTGGAAGGNC	TCCAGTCAGG	CAGCCCTANA	540
AACTGGGGAA	AAAAGAAAAG	GACGCCCAN	CCCCCAGCTG	TGCANCTACG	CACCTCAACA	600
GCACAGGGTG	GCAGCAAAAA	AACCACTTTA	CTTGGCACA	AACAAAAACT	NGGGGGGGCA	660
ACCCCGGCAC	CCCNANGGG	GTAAACAGGA	ANCNGGNAA	CNTGGAACCC	AATTNAGGCA	720
GGCCCNCCAC	CCCNAATNTT	GCTGGAAAT	TTTCCTCCC	CTAAATTNTT	TC	772

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCAATT	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTGGAT	GTCATAACAA	60
AGCTGATTGA	AGCAACCCTC	TACTTTTG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTCA	120
TTGGCTGTGT	TGGTGACGTT	GTCATTGCAA	CAGAATGGGG	GAAAGGCAC	GTTCTCTTG	180
AAGTANGGTG	AGTCCTCAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCATT	GAGCCCTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCTGGAAC	CATAATCTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCAG	GGAAAGTGCTC	AGCCATTGTG	GTGTACACCA	AGGCGACCAC	360
AGCAGCTGCN	ACCTCAGCAA	TGAAGATGAN	GAGGANGATG	AAGAAGAACG	TCNCGAGGGC	420
ACACTTGCTC	TCAGTCTTAN	CACCATANCA	GCCCNTGAAA	ACCAANANCA	AAGACCACNA	480
CNCCGGCTGC	GATGAAGAAA	TNACCCCNC	TTGACAAACT	TGCATGGCAC	TGGGANCCAC	540
AGTGGCCCNA	AAAATCTTCA	AAAAGGATGC	CCCATCNATT	GACCCCCCAA	ATGCCCACTG	600
CCAACAGGGG	CTGCCAACN	CNCNNAAACGA	TGANCCNATT	GNACAAGATC	TNCNTGGTCT	660
TNATNAACNT	GAACCTGCN	TNGTGGCTCC	TGTTCAAGNC	CNNGGCCTGA	CTTCTNAANN	720
AANGAACTCN	GAAGNCCCCA	CNGGANANN	G			751

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGGCG	TCCCTCTGCC	TGCCCACTCA	GTGGCAACAC	CCGGGAGCTG	TTTTGTCCTT	60
TGTGGANCCT	CAGCAGTNCC	CTCTTCAGA	ACTCANTGCC	AAGANCCCTG	AACAGGAGCC	120
ACCATGCACT	GCTTCAGCTT	CATTAAGACC	ATGATGATCC	TCTTCAATT	GCTCATCTTT	180
CTGTGTGGTG	CAGCCCTGTT	GGCAGTGGGC	ATCTGGGTGT	CAATCGATGG	GGCATCCTT	240
CTGAAGATCT	TCGGGCCACT	GTCGTCCAGT	GCCATGCAGT	TTGTCAACGT	GGGCTACTTC	300
CTCATCGCAG	CCGGCGTTGT	GGTCTTAGCT	CTAGGTTCC	TGGGCTGCTA	TGGTGCTAAG	360
ACTGAGAGCA	AGTGTGCCCT	CGTGACGTT	TTCTTCATCC	TCCTCCTCAT	CTTCATTGCT	420
GAGGTTGCAA	TGCTGTGGTC	GCCTTGGTGT	ACACCACAAT	GGCTGAGCAC	TTCCGTACGT	480
TGCTGGTAAT	GCCTGCCATC	AANAAAAGAT	TATGGGTTCC	CAGGAANACT	TCACTCAAGT	540
GTTGGAACAC	CACCATGAAA	GGGCTCAAGT	GCTGTGGCTT	CNNCCAACTA	TACGGATTT	600
GAAGANTCAC	CTACTTCAAA	GAAAANAGTG	CCTTCCCCC	ATTCTGTTG	CAATTGACAA	660
ACGTCCCCAA	CACAGCCAAT	TGAAAACCTG	CACCCAAACCC	AAANGGGTCC	CCAACCANAA	720
ATTNAAGGG						729

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCTTCCT	CAAAGTTGTT	CTTGTGCCA	TAACAACCAC	CATAGGTAAA	GCGGGCGCAG	60
TGTTCGCTGA	AGGGGTTGTA	GTACCAGCGC	GGGATGCTCT	CCTTGCAGAG	TCCTGTGTCT	120
GGCAGGTCCA	CGCAGTGCCC	TTTGTCACTG	GGGAAATGGA	TGCGCTGGAG	CTCGTCAAAG	180
CCACTCGTGT	ATTTTCACA	GGCAGCCTCG	TCCGACGCGT	CGGGGCAGTT	GGGGGTGTCT	240
TCACACTCCA	GGAAACTGTC	NATGCAGCAG	CCATTGCTGC	AGCGGAAC	GGTGGGCTGA	300

CANGTGCAG	AGCACACTGG	ATGGCGCCTT	TCCATGNNAN	GGGCCCTGNG	GGAAAGTCCC	360
TGANCCCCAN	ANCTGCCTCT	CAAANGCCCC	ACCTTGCACA	CCCCGACAGG	CTAGAATGGA	420
ATCTTCTTCC	CGAAAGGTAG	TTNTTCTTGT	TGCCCAANCC	ANCCCCNTAA	ACAAACTCTT	480
GCANATCTGC	TCCGNGGGGG	TCNTANTACC	ANCGTGGGAA	AAGAACCCCA	GGCNGCGAAC	540
CAANCTTGT	TGGATNCGAA	GCNATAATCT	NCTNTTCTGC	TTGGTGGACA	GCACCANTNA	600
CTGTNNANCT	TTAGNCCNTG	GTCCTCNTGG	GTTGNNTTG	AACCTAATCN	CCNNNTCAACT	660
GGGACAAGGT	AANTNGCCNT	CCTTTNAATT	CCCNANCNTN	CCCCCTGGTT	TGGGGTTTTN	720
CNCNCTCCTA	CCCCAGAAAN	NCCGTGTTCC	CCCCCAACTA	GGGGCCNAAA	CCNNTNTTC	780
CACAACCCTN	CCCCACCCAC	GGGTTCNGNT	GGTTNG			816

## (2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGGCCTG	GGCAGGCATA	NACTTGAAGG	TACAACCCCA	GGAACCCCTG	GTGCTGAAGG	60
ATGTGGAAAA	CACAGATTGG	CGCCTACTGC	GGGGTGACAC	GGATGTCAGG	GTAGAGAGGA	120
AAGACCCAAA	CCAGGTGGAA	CTGTGGGGAC	TCAAGGAANG	CACCTACCTG	TTCCAGCTGA	180
CAGTGAUTAG	CTCAGACCAAC	CCAGAGGACA	CGGCCAACGT	CACAGTCACT	GTGCTGTCCA	240
CCAAGCAGAC	AGAAGACTAC	TGCCTCGCAT	CCAACAANGT	GGGTCGCTGC	CGGGGCTCTT	300
TCCCACGCTG	GTACTATGAC	CCCACGGAGC	AGATCTGCAA	GAGTTTCGTT	TATGGAGGCT	360
GCTTGGGCAA	CAAGAACAAAC	TACCTTCGGG	AAGAAGAGTG	CATTCTANCC	TGTCNGGGTG	420
TGCAAGGTGG	GCCTTGANA	NGCANCTCTG	GGGCTCANGC	GACTTCCCC	CAGGGCCCT	480
CCATGGAAAG	GCGCCATCCA	NTGTTCTCTG	GCACCTGTCA	GCCCACCCAG	TTCCGCTGCA	540
NCAATGGCTG	CTGCATCNAC	ANTTCCCTNG	AATTGTGACA	ACACCCCCCA	NTGCCCCCAA	600
CCCTCCCAAC	AAAGCTTCCC	TGTTAAAAAA	TACNCCANTT	GGCTTTNAC	AAACNCCCGG	660
CNCCTCCNTT	TTCCCCNNTN	AACAAAGGGC	NCTNGCNTT	GAACTGCCCN	AACCCNGGAA	720
TCTNCCNNGG	AAAAANTNCC	CCCCCTGGTT	CCTNNAANCC	CCTCCNCNAA	ANCTNCCCCC	780
CCC						783

## (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCCCAATT	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCCCTC	TACTTTGG	TCGTGAGCCT	TTGCTTGGT	GCAGGTTCA	120
TTGGCTGTGT	TGGTGACGTT	GTCATTGCAA	CAGAATGGGG	GAAAGGCAC	GTTCTCTTG	180
AAGTAGGGTG	AGTCCTCAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCTGGGAAC	CATAATCTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCAG	GAAGTGCTCA	GCCATTGTGG	TGTACACCAA	GGCGACCAC	360
GCAGCTGCAA	CCTCAGCAAT	GAAGATGAGG	AGGAGGATGA	AGAAGAACGT	CNCGAGGGCA	420
CACTTGCTCT	CCGTCTTAGC	ACCATAGCAG	CCCANGAAAC	CAAGAGCAA	GACCACAAAC	480
CCNGCTGCGA	ATGAAAGAAA	NTACCCACGT	TGACAAACTG	CATGGCCACT	GGACGACAGT	540

TGGCCCGAAN	ATCTTCAGAA	AAGGGATGCC	CCATCGATTG	AACACCCANA	TGCCCACTGC	600
CNACAGGGCT	GCNCNCNCN	GAAAGAATGA	GCCATTGAAG	AAGGATCNTC	NTGGTCTTAA	660
TGAAC TGAAA	CCNTGCATGG	TGGCCCCTGT	TCAGGGCTCT	TGGCAGTGAA	TTCTGANAAA	720
AAGGAACNGC	NTNAGCCCCC	CCAAANGANA	AAACACCCCC	GGGTGTTGCC	CTGAATTGGC	780
GGCCAAGGAN	CCCTGCCCN	G				801

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGAGAGCCA	GGCGTCCCTC	TGCCTGCCA	CTCAGTGGCA	ACACCCGGGA	GCTGTTTGT	60
CCTTTGTGGA	GCCTCAGCAG	TTCCCTCTT	CAGAACTCAC	TGCCAAGAGC	CCTGAACAGG	120
AGCCACCATG	CAGTGCITCA	GCTTCATTAA	GACCATGATG	ATCCTCTTCA	ATTTGCTCAT	180
CTTTCTGTGT	GGTGCAGCCC	TGTTGGCAGT	GGGCATCTGG	GTGTCAATCG	ATGGGGCATC	240
CTTTCTGAAG	ATCTTCGGGC	CACTGTCGTC	CAGTGCATG	CAGTTGTCA	ACGTGGGCTA	300
CTTCCTCATC	GCAGCCGGCG	TTGTGGTCTT	TGCTCTTGGT	TTCCCTGGCT	GCTATGGTGC	360
TAAGACGGAG	AGCAAGTGTG	CCCTCGTGAC	GTTCTTCTTC	ATCCTCCTCC	TCATCTTCAT	420
TGCTGAAGTT	GCAGCTGCTG	TGGTCGCCTT	GGTGTACACC	ACAATGGCTG	AACCATTCT	480
GACGTTGCTG	GTANTGCCTG	CCATCAANAA	AGATTATGGG	TTCCCAGGAA	AAATTCACTC	540
AANTNTGGAA	CACCNCCATG	AAAAGGGCTC	CAATTCTGN	TGGCTTCCCC	AACTATACCG	600
GAATTGGAA	AGANTCNC	TACTTCCAAA	AAAAAANANT	TGCCTTNCC	CCCNNTCTGT	660
TGCAATGAAA	ACNTCCCAAN	ACNGCCAATN	AAAACCTGCC	CNNCAAAAA	GGNTCNAAA	720
CAAAAAAANT	NNAAGGGTTN					740

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCGCTGGTTG	CGCTGGTCCA	GNGNAGCCAC	GAAGCACGTC	AGCATAACACA	GCCTCAATCA	60
CAAGGTCTTC	CAGCTGCCGC	ACATTACGCA	GGGCAAGAGC	CTCCAGCAAC	ACTGCATATG	120
GGATAACACTT	TACTTTAGCA	GCCAGGGTGA	CAACTGAGAG	GTGTGAGAC	TTATTCTTCT	180
GAGCCTCTGT	TAGTGGAGGA	AGATTCGGG	CTTCAGCTAA	GTAGTCAGCG	TATGTCCCAT	240
AAGCAAACAC	TGTGAGCAGC	CGGAAGGTTAG	AGGCAAAGTC	ACTCTCAGCC	AGCTCTCTAA	300
CATTGGGCAT	GTCCAGCAGT	TCTCCAAACA	CGTAGACACC	AGNGGCCTCC	AGCACCTGAT	360
GGATGAGTGT	GGCCAGCGCT	GCCCCCTTGG	CCGACTTGGC	TAGGAGCAGA	AATTGCTCCT	420
GGTTCTGCC	TGTCACCTTC	ACTTCCGCAC	TCATCACTGC	ACTGAGTGTG	GGGGACTTGG	480
GCTCAGGATG	TCCAGAGACG	TGGTTCCGCC	CCCTCNCTTA	ATGACACCGN	CCANNCAACC	540
GTCGGCTCCC	GCCGANTGNG	TTCGTCGTNC	CTGGGTCAAG	GTCTGCTGGC	CNCTACTTGC	600
AANCTTCGTC	NGGCCCATGG	AATTCAACCNC	ACCGGAACTN	GTANGATCCA	CTNNTTCTAT	660
AACCAGGNCGC	CACCGCNNNT	GGAACTCCAC	TCTTNTTNCC	TTTACTTGAG	GGTTAAGGTC	720
ACCCTTNNGC	TTACCTTGGT	CCAAACCNTN	CCNTGTGTG	ANATNGTNA	TCNGGNCCNA	780
TNCCANCCNC	ATANGAAGCC	NG				802

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CNAAGCTTCC	AGGTNACGGG	CCGCNAANCC	TGACCCNAGG	TANCANAANG	CAGNCNGCGG	60
GAGCCCACCG	TCACCGNGNG	GNGTCTTAT	NGGAGGGGGC	GGAGCCACAT	CNCTGGACNT	120
CNTGACCCCA	ACTCCCCNCC	NCNCANTGCA	GTGATGAGTG	CAGAACTGAA	GGTNACGTGG	180
CAGGAACCAA	GANCAAANN	TGCTCCNNTC	CAAGTCGGCN	NAGGGGGCGG	GGCTGGCCAC	240
GCNCATCCNT	CNAGTGCTGN	AAAGCCCCNN	CCTGTCTACT	TGTTTGGAGA	ACNGCENNNGA	300
CATGCCAGN	GTTANATAAC	NGGCNGAGAG	TNANTTTGCC	TCTCCCTTCC	GGCTGCGCAN	360
CGNGTNTGCT	TAGNGGACAT	AACCTGACTA	CTTAACTGAA	CCCNNGAATC	TNCCNCCCCCT	420
CCACTAAGCT	CAGAACAAAAA	AACTTCGACA	CCACTCANTT	GTCACCTGNC	TGCTCAAGTA	480
AAGTGTACCC	CATNCCCAAT	GTNTGCTNGA	NGCTCTGNCC	TGCNTTANGT	TCGGTCCTGG	540
GAAGACCTAT	CAATTNAAGC	TATGTTCTG	ACTGCCTCTT	GCTCCCTGNA	ACAANCNACC	600
CNNCNNTCCA	AGGGGGGGNC	GGCCCCCAAT	CCCCCCAACC	NTNAATTNAN	TTTANCCCN	660
CCCCCNGGCC	CGGCCTTTA	CNANCNTCNN	NNACNGGGNA	AAACCNNNGC	TTTNCCCAAC	720
NNAATCCNCC	T					731

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTTTTTTTT	TTTTTTTTTT	TAAAAACCCC	CTCCATTNAA	TGNAAACTTC	CGAAATTGTC	60
CAACCCCCTC	NTCCAAATNN	CCNTTCCGG	GNGGGGTTC	CAAACCCAAN	TTANNTTTGG	120
ANNTTAAATT	AAATNTTNNT	TGGNGGNNA	ANCCNAATGT	NANGAAAGTT	NAACCCANTA	180
TNANCTNAA	TNCCTGGAAA	CCNGTNGNTT	CCAAAAATNT	TTAACCTTA	ANTCCCTCCG	240
AAATNGTTNA	NGGAAAACCC	AANTTCTCNT	AAGGTTGTTT	GAAGGNTNAA	TNAAAANCCC	300
NNCCAATTGT	TTTNGCCAC	GCCTGAATTA	ATTGGNTTCC	GNTGTTTCC	NTTAAAANAA	360
GGNNANCCCC	GGTTANTNAA	TCCCCCCNNC	CCCAATTATA	CCGANTTTT	TTNGAATTGG	420
GANCCCNCGG	GAATTAACGG	GGNNNNNTCCC	TNTTGGGGGG	CNGGNCCCC	CCCCNTCGGG	480
GGTTNGGGNC	AGGNCNNAAT	TGTTTAAGGG	TCCGAAAAAT	CCCTCCNAGA	AAAAAAANCTC	540
CCAGGNTGAG	NNTNGGGTTT	NCCCCCCCCC	CANGGCCCT	CTCGNANAGT	TGGGGTTTGG	600
GGGGCCTGGG	ATTTNTTTTC	CCCTNTTNCC	TCCCCCCCCC	CCNGGGANAG	AGGTTNGNGT	660
TTTGNTCNNC	GGCCCCNCCN	AAGANTTTN	CCGANTTNAN	TTAAATCCNT	GCCTNGGCNA	720
AGTCCNTTGN	AGGGNTAAAN	GGCCCCCTNN	CGGG			754

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCANCCAT	GACCCNAAC	NNGGACCNC	TCANCCGGNC	NNNCNACCNC	CGGCCNATCA	60
NNGTNAGNNC	ACTNCNNTN	NATCACNCCC	CNCCNACTAC	GCCCNCNANC	CNAAGCNCTA	120
NNCANATNCC	ACTGANNGCG	CGANGTNGAN	NGAGAAANCT	NATACCANAG	NCACCCANACN	180
CCAGCTGTCC	NANAANGCCT	NNNATACNGG	NNNATCCAAT	NTGNANCCTC	CNAAGTATTN	240
NNCNNCANAT	GATTTCCTN	ANCCGATTAC	CCNTNCCCC	TANCCCCTCC	CCCCAACNA	300
CGAAGGCNCT	GGNCCNAAGG	NNGCGNCNCC	CCGCTAGNTC	CCCNNAAGT	CNCNCNCCTA	360
AACTCANCCN	NATTACNCGC	TTCNTGAGTA	TCACTCCCCG	AATCTCACCC	TACTCAACTC	420
AAAAANATCN	GATACAAAAT	AATNCAAGCC	TGNTTATNAC	ACTNTGACTG	GGTCTCTATT	480
TTAGNGGTCC	NTNAANCNTC	CTAATACTTC	CAGTCTNCCT	TCNCCAATT	CCNAANGGCT	540
CTTCNGACA	GCATNTTTG	GTTCCCNNTT	GGGTTCTTAN	NGAATTGCC	TTCNTNGAAC	600
GGGCTCNTCT	TTTCCTTCGG	TTANCCTGGN	TTCNNCCGGC	CAGTTATTAT	TTCCCNTTTT	660
AAATTCTNCC	CNTTANTTT	TGGCNTTCNA	AACCCCCGGC	CTTGAAAACG	GCCCCCTGGT	720
AAAAGGTTGT	TTTGANAAAA	TTTTGTTTT	GTTCC			755

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 849 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTTTTTT	TTTTTANGTG	TNGTCGTGCA	GGTAGAGGCT	TACTACAANT	GTGAANACGT	60
ACGCTNGGAN	TAANGCGACC	CGANTTCTAG	GANNCCCT	AAAATCANAC	TGTGAAGATN	120
ATCCTGNNA	CGGAANGGTC	ACCGGNNGAT	NNTGCTAGGG	TGNCCNCTCC	CANNNCNTTN	180
CATAACTCNG	NGGCCCTGCC	CACCACCTTC	GGCGGCCNG	NGNCCGGGCC	CGGGTCATTN	240
GNNTTAACCN	CACTNNGCNA	NCGGTTCCN	NCCCCNNCNG	ACCCNGGCGA	TCCGGGGTNC	300
TCTGTCTTCC	CCTGNAGNCN	ANAAANTGGG	CCNCGGNCCC	CTTTACCCCT	NNACAAGCCA	360
CNGCCNTCTA	NCCNCNGCCC	CCCCTCCANT	NNGGGGACT	GCCNANNNGCT	CCGTTNCTNG	420
NNACCCNNN	GGGTNCCTCG	GTTGTCGANT	CNACCGNANG	CCANGGATT	CNAAGGAAGG	480
TGCGTTNTTG	GCCCCTACCC	TTCGCTNCGG	NNCACCCCTC	CCGACNANGA	NCCGCTCCCG	540
CNCNNCGNNG	CCTCNCTCG	CAACACCCGC	NCTCNTCNGT	NCGGNNNCC	CCCCACCCGC	600
NCCCTCNCNC	NGNCGNACN	CTCCNCCNCC	GTCTCANNCA	CCACCCGCC	CCGCCAGGCC	660
NTCANCCACN	GGNNGACNNG	NAGNCNNNTC	GCNCAGCGCN	GCGNCNCCT	CGCCNCNGAA	720
CTNCNTCNGG	CCANTNNCGC	TCAANCCNNA	CNAACGCCG	CTGCGCGGCC	CGNAGCGNCC	780
NCCTCCNCGA	GTCCTCCCGN	CTTCCNACCC	ANGNNTTCCN	CGAGGACACN	NNACCCGCC	840
NNCANGCGG						849

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 872 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGCAAAC	TA	CTTCGCTC	GNACTCGTGC	GCCTCGCTNC	TCTTTCC	TC	CGCAACC	ATG	60
TCTGACNANC	CCGATTNGGC	NGATATCNAN	AAGNTCGANC	AGTCCAA	ACT	GANTAAC	ACA	120	
CACACNCNAN	AGANAAATCC	NCTGCCTTC	ANAGTANACN	ATTGAAC	NNG	AGAAC	CANGC	180	
NGGCGAATCG	TAATNAGGCG	TGCGCCGCCA	ATNTGTCNCC	GTTTATTNTN	CCAGC	NTC	NC	240	
CTNCCNACCC	TACNTCTTC	NAGCTGTCNN	ACCCCTNGTN	CGNACCCCC	NAGGT	CGGGA	300		
TCGGGTTTNN	NNTGACCGNG	CNNCCCTCC	CCCCNTCCAT	NACGANCC	CCG	CACC	ACC	360	
NANNGNCNGC	NCCCCNNCT	CTTCGCCNCC	CTGTCCTNTN	CCCCTGTNGC	CTGGC	N	CNGN	420	
ACCGCATTGA	CCCTCGCCNN	CTNCNNGAAA	NCGNANACGT	CGGGGTTGNN	ANNAN	CGCTG	480		
TGGGNNNNGCG	TCTGCNCCGC	GTTCC	TCNNCTTCCA	CCATCTTCNT	TACNGGG	TCT	540		
CCNCGCCNTC	TCNNNCACNC	CCTGGGACGC	TNTCCTNTGC	CCCCCTTNAC	TCCCC	CCC	CTT	600	
CGNCGTGNCC	CGNCCCCACC	NTCATT	TCNNNTNCA	NACGNTCTTC	ACAANNN	CCT	GGNTNN	660	
CNANCNGNCN	GTCANCCNAG	GGAAGGGNGG	GGNNCCNN	NTTGACGTTG	NGGNG	ANGTC	720		
CGAANANTCC	TCNCCNTCAN	CNCTACCCCT	CGGGCGNNCT	CTCNGTTNCC	AACTT	ANCAA	780		
NTCTCCCCCG	NGNGCNCNTC	TCAGCCTCNC	CCNCCCCNCT	CTCTGCANTG	TNCTCTG	GCTC	840		
TNACCNNTAC	GANTNTTCGN	CNCCCTCTTT	CC					872	

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATGCAAGC	TTGAGTATT	C	TATAGNTCA	CCTAAATANC	TTGGC	NTAAT	CATGG	TNTA	60
NCTGNCTTCC	TGTGTCAAAT	G	TATACNAAN	TANATATGAA	TCTNAT	NTGAA	CAAGAN	NGTA	120
TCNTNCATTA	GTAACAANTG	T	NNNTGTCCAT	CCTGTCNGAN	CANATT	CCC	TNNATT	NCGN	180
CGCATT	GCNCANTATN	T	AAATNGGGAA	NTC	NNNTNNN	NCACC	NNCAT	CTATC	240
GCNCCTGAC	TGGNAGAGAT	G	GGATNANTTC	TNN	NTGACC	NACAT	GTTCA	TCTTG	300
AANAN	CGCNGNCCAC	G	CGGTTNGNNG	CNAGCC	NNTC	CCAAG	ACCTC	CTGTG	360
AACCT	TCGTC	A	AGANNCATCA	AAC	NTGGGAA	ACCCG	CNNCC	ANG	420
GATCCC	GTCC	G	AGGNTTNACC	ATCC	CTTCNC	AGCG	CCCCCT	GTG	480
GTGTC	CNANC	C	GTCAAACAT	GAN	ACGCGCC	AGN	CCANCCG	CAAT	540
GAAC	CCCCCTA	G	GGGGGANTNA	TN	CAAANCCC	CAGG	ATTGTC	CNC	600
CCC	CCNCTT	G	GGG	GTGACC	A	ANT	CCC	GG	660
CCC	ACCGG	G	GGG	GAANCT	C	GN	NTC	GG	720
ACC	GGNC	C	GGN	GAANNG	A	NC	NTC	GG	780
NCC	ACNG	N	AGNT	CCCC	C	NGG	GTN	CG	815

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGAGATGTC	TCGCTCCGTG	GCCTTAGCTG	TGCTCGCGCT	ACTCTCTCTT	TCTGGCCTGG	60
AGGCTATCCA	GCGTACTCCA	AAGATTCAAGG	TTTACTCACG	TCATCCAGCA	GAGAATGGAA	120
AGTCAAATT	CCTGAATTGC	TATGTGTCTG	GGTTTCATCC	ATCCGACATT	GAANTTGACT	180
TACTGAAGAA	TGGANAGAGA	ATTGAAAAAG	TGGAGCATTC	AGACTTGTCT	TTCAGCAAGG	240
ACTGGTCTT	CTATCTCNTG	TACTACACTG	AATTCAACCC	CACTGAAAAA	GATGAGTATG	300
CCTGCCGTGT	GAACCATGTG	ACTTGTAC	AGCCCAAGAT	AGTTAAGTGG	GATCGAGACA	360
TGTAAGCAGN	CNNCATGGAA	GTGGAAGAT	GCCGCATTG	GATTGGATGA	ATTCCAAATT	420
CTGCTTGCTT	GCNTTTAAT	ANTGATATGC	NTATACACCC	TACCCTTAT	GNCCCCAAAT	480
TGTAGGGGTT	ACATNANTGT	TCNCNTNGGA	CATGATCTTC	CTTTATAANT	CCNCCNTTCG	540
AATTGCCCGT	CNCCCNGTN	NGAATGTTTC	CNNAACCACG	GTTGGCTCCC	CCAGGTCNCC	600
TCTTACGGAA	GGGCCTGGGC	CNCTTNCAA	GGTTGGGGGA	ACCNAAAATT	TCNCTNTGC	660
CCNCCCNCCA	CNNCTTGNG	NNCNCANTTT	GGAACCCTTC	CNATTCCCCT	TGGCCTCNNA	720
NCCTTNNCTA	ANAAAACCTN	AAANCGTNGC	NAAANNTTN	ACTTCCCCCC	TTACC	775

## (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 820 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ANATTANTAC	AGTGTAAATCT	TTTCCCAGAG	GTGTGTANAG	GGAACGGGGC	CTAGAGGCAT	60
CCCANAGATA	NCTTATANCA	ACAGTGCTTT	GACCAAGAGC	TGCTGGGCAC	ATTTCCTGCA	120
GAAAAGGTGG	CGGTCCCCAT	CACTCCTCCT	CTCCCATAGC	CATCCCAGAG	GGGTGAGTAG	180
CCATCANGCC	TTCGGTGGGA	GGGAGTCANG	GAAACAACAN	ACCACAGAGC	ANACAGACCA	240
NTGATGACCA	TGGGCGGGAG	CGAGCCTCTT	CCCTGNACCG	GGGTGGCANA	NGANAGCCTA	300
NCTGAGGGGT	CACACTATAA	ACGTTAACGA	CCNAGATNAN	CACCTGCTTC	AAGTGCACCC	360
TTCCTACCTG	ACNACCAGNG	ACCNNAACT	GCNGCCTGGG	GACAGCNCTG	GGANCAGCTA	420
ACNNAGCACT	CACCTGCC	CCCATGGCCG	TNCGCNTCCC	TGGTCCTGNC	AAGGGAAGCT	480
CCCTGTTGGA	ATTNCGGGG	NACCAAGGG	NCCCCCTCCT	CCANCTGTGA	AGGAAAANN	540
GATGGAATT	TNCCCTCCG	GCCNNTCCCC	TCTTCCTTTA	CACGCCCCCT	NNTACTCNC	600
TCCCTCTNTT	NTCCTGNCNC	ACTTTTNACC	CCNNNATTTC	CCTTNATTGA	TCGGANNCTN	660
GANATTCCAC	TNNCGCCTNC	CNTCNATCNG	NAANACNAAA	NACTNTCTNA	CCCNNGGGAT	720
GGGNNCCTCG	NTCATCCTCT	CTTTTCNCT	ACCNCCNNT	CTTGCCTCT	CCTTNGATCA	780
TCCAACCNTC	GN	GGCCNTN	CCCCCCCCNNN	TCCTTTNCCC		820

## (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 818 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGGGTGAT	GGCCTCTTCC	TCCTCAGGG	CCTCTGACTG	CTCTGGGCCA	AAGAATCTCT	60
TGTTTCTTCT	CCGAGCCCCA	GGCAGCGGTG	ATTCAAGCCCT	GCCCAACCTG	ATTCTGATGA	120
CTGCGGATGC	TGTGACGGAC	CCAAGGGCA	AATAGGGTCC	CAGGGTCCAG	GGAGGGGGCGC	180
CTGCTGAGCA	CTTCCGCCCC	TCACCCCTGCC	CAGCCCCTGC	CATGAGCTCT	GGGCTGGGTC	240
TCCGCCTCCA	GGGTTCTGCT	CTTCCANGCA	NGCCANCAAG	TGGCGCTGGG	CCACACTGGC	300

TTCTTCCTGC	CCCNTCCCTG	GCTCTGANTC	TCTGTCTTCC	TGTCCTGTGC	ANGNCNCCTTG	360
GATCTCAGTT	TCCCTCNCTC	ANNGAACTCT	GTTTCTGANN	TCTTCANTTA	ACTNTGANTT	420
TATNACCNAN	TGGNCTGTNC	TGTCNNACTT	TAATGGGCCN	GACCGGCTAA	TCCCTCCCTC	480
NCTCCCTTCC	ANTTCNNNA	ACCNNGCTNC	CNTCNTCTCC	CCNTANCCCG	CCNGGGAAANC	540
CTCCTTGCC	CTNACCANGG	GCCNNNACCG	CCCNTNNCTN	GGGGGGCNG	GTNNCTNCNC	600
CTGNTNNCCC	CNCTCNCNNT	TNCCTCGTCC	CNNCNNGCNC	NNGCANNTTC	NCNGTCCCNN	660
TNNCTCTCN	NGTNTCGNAA	NGNTCNCNTN	TNNNNNGNCN	NGNTNNTNCN	TCCCTCTCNC	720
CNNNTGNANG	TNNTTNNNNC	NCNGNNCCCC	NNNCNNNNNN	NGGNNNTNNN	TCTNCNCNGC	780
CCCNCCCCC	NGNATTAAGG	CCTCCNNTCT	CCGGCCNC			818

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGAAGGGCG	GAGGGATATT	GTANGGGATT	GAGGGATAGG	AGNATAANGG	GGGAGGTGTG	60
TCCCAACATG	ANGGTGNNGT	TCTCTTTGA	ANGAGGGTTG	NGTTTTANN	CCNGGTGGGT	120
GATTNAACCC	CATTGTATGG	AGNAAAGGN	TTTNAGGGAT	TTTCGGCTC	TTATCAGTAT	180
NTANATTCC	GTNAATCGGA	AAATNATNTT	TCNNCNGGAA	AATNTTGCTC	CCATCCGNAA	240
ATTNCTCCCG	GGTAGTGCAT	NTTNGGGGN	CNGCCANGTT	TCCCAGGCTG	CTANAATCGT	300
ACTAAAGNTT	NAAGTGGGAN	TNCAAATGAA	AACCTNNCAC	AGAGNATCCN	TACCCGACTG	360
TNNNTTNCC	TCGCCCTNTG	ACTCTGCNNG	AGCCAATAC	CCNNGNGNAT	GTCNCCNGN	420
NNNGCGNCNC	TGAAANNNNC	TCGNGGCTNN	GANCATCANG	GGGTTTCGCA	TCAAAAGCNN	480
CGTTTCNCAT	NAAGGCACTT	TNGCCTCATC	CAACCNCNTNG	CCCTCNCNNCA	TTTNGCCGTC	540
NGGTTCNCC	ACGCTNNTNG	CNCCTNNNTN	GANATTTCNC	CCGCCTNGGG	NAANCCTCCT	600
GNAATGGGT	GGGNCTTNTC	TTTNACCNN	GNGGTNTACT	AATCNNCTNC	ACGCNTNCTT	660
TCTCNACCCCC	CCCCCTTTT	CAATCCCANC	GGCNAATGGG	GTCTCCCCNN	CGANGGGGG	720
NNNCCCANNC	C					731

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGGNCNC	TTCTATGANT	ANTNTTAGAT	60
CGCTCANACC	TCACANCCTC	CCNACNANGC	CTATAANGAA	NANNAATAGA	NCTGTNCNN	120
ATNTNTACNC	TCATANNCT	CNNNACCCAC	TCCCTCTTAA	CCCNACTGT	GCCTATNGCN	180
TNNCTANTCT	NTGCCGCCTN	CNANCCACCN	GTGGGCCNAC	CNCNNGNATT	CTCNATCTCC	240
TCNCCATNTN	GCCTANANTA	NGTNCATACC	CTATACCTAC	NCCAATGCTA	NNNCTAANCN	300
TCCATNANTT	ANNNTAACTA	CCACTGACNT	NGACTTTNC	ATNANCTCCT	AATTGAAATC	360
TACTCTGACT	CCCACNGCCT	ANNNATTAGC	ANCNTCCCC	NACNATNTCT	CAACCAAATC	420
NTCAACAAACC	TATCTANCTG	TTCNCCAACC	NTTNCCTCCG	ATCCCCNNAC	AACCCCCCTC	480
CCAAATACCC	NCCACCTGAC	NCCTAACCN	CACCATCCCG	GCAAGCCNAN	GGNCATTAN	540
CCACTGGAAT	CACNATNGGA	NAAAAAAAAC	CCNAACTCTC	TANCNCNNAT	CTCCCTAANA	600

AATNCTCCTN	NAATTACTN	NCANTNCCAT	CAANCCCACN	TGAAACNNAA	CCCCTGTTT	660
TANATCCCTT	CTTTCGAAAAA	CCNACCCTT	ANNNCCCAAC	CTTNGGGCC	CCCCCNCTNC	720
CCNAATGAAG	GNCNCCAAT	CNANGAAACG	NCCNTGAAAAA	ANCNAGGCNA	ANANNNTCCG	780
CANATCCTAT	CCCTTANTTN	GGGNCCCTT	NCCCNNGGCC	CC		822

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGCCGCCTG	CTCTGGCACA	TGCCTCCTGA	ATGGCATCAA	AAGTGATGGA	CTGCCATTG	60
CTAGAGAAGA	CCTTCTCTCC	TACTGTCATT	ATGGAGCCCT	GCAGACTGAG	GGCTCCCCCT	120
GTCTGCAGGA	TTTGATGTCT	GAAGTCGTGG	AGTGTGGCTT	GGAGCTCCTC	ATCTACATNA	180
GCTGGAAGCC	CTGGAGGGCC	TCTCTCGCCA	GCCTCCCCCT	TCTCTCCACG	CTCTCCANGG	240
ACACCAGGGG	CTCCAGGCAG	CCCATTATTC	CCAGNANGAC	ATGGTGTTC	TCCACGCGGA	300
CCCATGGGGC	CTGNAAGGCC	AGGGTCTCCT	TTGACACCAT	CTCTCCCGTC	CTGCCTGGCA	360
GGCCGTGGGA	TCCACTANTT	CTANAACGGN	CGCCACCNCG	GTGGGAGCTC	CAGCTTTGT	420
TCCCNTTAAT	GAAGGTTAAT	TGCNCGCTTG	GCGTAATCAT	NGGTCANAAC	TNTTCCTGT	480
GTGAAATTGT	TTNTCCCCTC	NCNATTCCNC	NCNACATACN	AACCCGGAAN	CATAAAGTGT	540
TAAAGCCTGG	GGGTNGCCTN	NNGAATNAAC	TNAACTCAAT	TAATTGCGTT	GGCTCATGGC	600
CCGCTTTCCN	TTCNGGAAAAA	CTGTCNTCCC	CTGCNTTNNT	GAATCGGCCA	CCCCCNNGGG	660
AAAAGCGGTT	TGCNTTTNG	GGGGNTCCTT	CCNCTTCCCC	CCTCNCTAAN	CCCTNCGCCT	720
CGGTCGTTNC	NGGTNGCGGG	GAANGGNAT	NNNCTCCNC	NAAGGGGNG	AGNNNGNTAT	780
CCCCAAA						787

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTTTTTT	TTTTTTGGC	GATGCTACTG	TTTAATTGCA	GGAGGTGGGG	GTGTGTGTAC	60
CATGTACCAAG	GGCTATTAGA	AGCAAGAAGG	AAGGAGGGAG	GGCAGAGCGC	CCTGCTGAGC	120
AACAAAGGAC	TCCTGCAGCC	TTCTCTGTCT	GTCTCTTGGC	GCAGGCACAT	GGGGAGGCCT	180
CCCGCAGGGT	GGGGGCCACC	AGTCCAGGGG	TGGGAGCACT	ACANGGGTG	GGAGTGGGTG	240
GTGGCTGGTN	CNAATGGCCT	GNACACANATC	CCTACGATTG	TTGACACCTG	GATTTCACCA	300
GGGGACCTTC	TGTTCTCCCA	NGGNAACTTC	NTNNATCTCN	AAAGAACACA	ACTGTTCTT	360
CNGCANTTCT	GGCTGTTCAT	GGAAAGCACA	GGTGTCCNAT	TTNGGCTGGG	ACTTGGTACA	420
TATGGTTCCG	GCCCACCTCT	CCCNTCNAAN	AAGTAATTCA	CCCCCCCCCN	CCNTCTNTTG	480
CCTGGGCCCT	TAANTACCCA	CACCGGAAC	CANTTANTTA	TTCATCTTNG	GNTGGGCTTG	540
NTNATCNCN	CCTGAANGCG	CCAAGTTGAA	AGGCCACGCC	GTNCCCNCTC	CCCATAGNAN	600
NTTTTNNCNT	CANCTAATGC	CCCCCNNGGC	AACNATCCAA	TCCCCCCCCN	TGGGGGCC	660
AGCCCANGGC	CCCCGNCTCG	GGNNNCCNGN	CNCGNANTCC	CCAGGNTCTC	CCANTCNGNC	720
CCNNNGCNCC	CCCGCACGCA	GAACANAAGG	NTNGAGCCNC	CGCANNNNNN	NGGTNNCNAC	780
CTCGCCCCCCC	CCNNCGNNG					799

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TTTTNCCNAG	GGCAGGTTA	TTGACAACCT	CNCGGGACAC	AANCAGGCTG	GGGACAGGAC	120
GGCAACAGGC	TCCGGCGGCG	GCGGCGGCGG	CCCTACCTGC	GGTACCAAAT	NTGCAGCCTC	180
CGCTCCCGCT	TGATNTTCCT	CTGCAGCTGC	AGGATGCCNT	AAAACAGGGC	CTCGGCCNTN	240
GGTGGGCACC	CTGGGATTN	AATTCCACG	GGCACAAATGC	GGTCGCANCC	CCTCACCACC	300
NATTAGGAAT	AGTGGTNTTA	CCCNCNCNC	TTGGCNCACT	CCCCNTGGAA	ACCACTTNTC	360
GC GGCTCCGG	CATCTGGTCT	TAAACCTTGC	AAACNCTGGG	GCCCTCTTT	TGGTTANTNT	420
NCCNGCCACA	ATCATNACTC	AGACTGGCNC	GGGCTGGCCC	AAAAAAANCN	CCCCAAAACC	480
GGNCCATGTC	TTNNCGGGGT	TGCTGCNATN	TNCATCACCT	CCCAGGCNCA	NCAGGNCAAC	540
CCAAAAGTTC	TTGNGGCCCN	CAAAAAANCT	CCGGGGGGNC	CCAGTTCAA	CAAAGTCATC	600
CCCCTTGGCC	CCCAAATCCT	CCCCCGNTT	NCTGGGTTTG	GGAACCCACG	CCTCTNNCTT	660
TGGNNGGCAA	GNTGGNTCCC	CCTTCGGGCC	CCCGGTGGGC	CCNNCTCTAA	NGAAAACNCC	720
NTCCTNNNCA	CCATCCCCCC	NNGNNAACGNC	TANCAANGNA	TCCCTTTTT	TANAAACGGG	780
CCCCCCNCG						789

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGAACAT	GTTGGATGGT	GGAGCACCTT	TCTATACGAC	TTACAGGACA	GCAGATGGGG	60
AATTCAATGGC	TGTTGGAGCA	ATANAACCCC	AGTTCTACGA	GCTGCTGATC	AAAGGACTTG	120
GACTAAAGTC	TGATGAACCT	CCCAATCAGA	TGAGCATGGA	TGATTGGCCA	GAAATGAANA	180
AGAAGTTGC	AGATGTATTT	GCAAAGAAGA	CGAAGGCAGA	GTGGTGTCAA	ATCTTGACG	240
GCACAGATGC	CTGTGTACT	CCGGTTCTGA	CTTTGAGGA	GGTTGTTCAT	CATGATCACA	300
ACAANGAACG	GGGCTCGTTT	ATCACCANTG	AGGAGCAGGA	CGTGAGCCCC	CGCCCTGCAC	360
CTCTGCTGTT	AAACACCCCCA	GCCATCCCTT	CTTCAAAAG	GGATCCACTA	CTTCTAGAGC	420
GGNCGCCACC	GCGGTGGAGC	TCCAGCTTT	GTTCCCTTA	GTGAGGGTTA	ATTGCGCGCT	480
TGGCGTAATC	ATGGTCATAN	CTGTTTCCTG	TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	540
ACAACATACG	ANCCCGAAGC	ATNAAATTCT	AAAGCCTGGN	GGTNGCCTAA	TGANTGAACT	600
NACTCACATT	AATTGGCTTT	GCGCTCACTG	CCCGCTTTCC	AGTCCGGAAA	ACCTGTCCTT	660
GCCAGCTGCC	NTTAATGAAT	CNGGCCACCC	CCCGGGGAAA	AGGCNGTTG	CTTNTTGGGG	720
CGCNCTTCCC	GCTTCTCGC	TTCCCTGAANT	CCTTCCCCCC	GGTCTTTCGG	CTTGCAGGCNA	780
ACGGTATCNA	CCT					793

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCGCGACCG	GCATGTACGA	GCAACTCAAG	GGCGAGTGG	ACCGTAAAAG	CCCCAATCTT	60
ANCAAGTGCG	GGGAANAGCT	GGGTCGACTC	AAGCTAGTTC	TTCTGGAGCT	CAACTTCTTG	120
CCAACCACAG	GGACCAAGCT	GACCAAACAG	CAGCTAATT	TGGCCCGTGA	CATACTGGAG	180
ATCGGGGCC	AATGGAGCAT	CCTACGCAAN	GACATCCCCT	CCTTCGAGCG	CTACATGGCC	240
CAGCTCAAAT	GCTACTACTT	TGATTACAAN	GAGCAGCTCC	CCGAGTCAGC	CTATATGCAC	300
CAGCTCTTGG	GCCTCAACCT	CCTCTTCCTG	CTGTCCCAGA	ACCGGGTGGC	TGANTNCCAC	360
ACGGANTTGG	ANCGGCTGCC	TGCCCAANGA	CATACANACC	AATGTCTACA	TCNACCACCA	420
GTGTCTGG	GCAATACTGA	TGGANGGCAG	CTACCNC	GTNTTCTGG	CCNAGGGTAA	480
CATCCCCCGC	CGAGAGCTAC	ACCTTCTTCA	TTGACATCCT	GCTCGACACT	ATCAGGGATG	540
AAAATCGCNG	GGTTGCTCCA	GAAAGGCTNC	AANAANATCC	TTTTCNCTGA	AGGCCCCCGG	600
ATNCNCTAGT	NCTAGAATCG	GCCGCCATC	GCGGTGGANC	CTCCAACCTT	TCGTTNCCCT	660
TTACTGAGGG	TTNATTGCCG	CCCTTGGCGT	TATCATGGTC	ACNCCNGTT	CCTGTGTTGA	720
AATTNTTAAC	CCCCCACAA	TCCACGCCNA	CATTNG			756

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 834 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGGATCTCT	ANATCNACCT	GNATGCATGG	TTGTCGGTGT	GGTCGCTGTC	GATGAANATG	60
AACAGGATCT	TGCCCTTGAA	GCTCTCGGCT	GCTGTNTTTA	AGTTGCTCAG	TCTGCCGTCA	120
TAGTCAGACA	CNCTCTTGGG	CAAAAAACAN	CAGGATNTGA	GTCTTGATT	CACCTCCAAT	180
AATCTCNGG	GCTGTCTGCT	CGGTGAACTC	GATGACNANG	GGCAGCTGGT	TGTGTNTGAT	240
AAANTCCANC	ANGTTCTCCT	TGGTGACCTC	CCCTTCAAAG	TTGTTCCGGC	CTTCATCAA	300
CTTCTNNAAN	ANGANNANCC	CANCTTGTC	GAGCTGGNAT	TTGGANAACA	CGTCACTGTT	360
GGAAACTGAT	CCCAAATGGT	ATGTCATCCA	TCGCCTCTGC	TGCCTGAAA	AAACTTGCTT	420
GGCNCAAATC	CGACTCCCCN	TCCTTGAAAG	AAGCCNATCA	CACCCCCCTC	CCTGGACTCC	480
NNCAANGACT	CTNCCGCTNC	CCCNTCCNNG	CAGGGTTGGT	GGCANNCCGG	GCCCNTGCGC	540
TTCTTCAGCC	AGTTCACNAT	NTTCATCAGC	CCCTCTGCCA	GCTGTTNTAT	TCCTTGGGGG	600
GGAANCCGTC	TCTCCCTTCC	TGAANNAACT	TTGACCGTNG	GAATAGCCGC	GCNTCNCNT	660
ACNTNCTGGG	CCGGGTTCAA	ANTCCCTCCN	TTGNCNNTCN	CCTCGGGCCA	TTCTGGATTT	720
NCCNAACTTT	TTCCTTCCCC	CNCCCCNCGG	NGTTGGNTT	TTTCATNGGG	CCCCAACTCT	780
GCTNTTGGCC	ANTCCCCTGG	GGGCNTNTAN	CNCCCCCTNT	GGTCCCNTNG	GGCC	834

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 814 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGNCGCTT	CCNGCCGCGC	CCC GTTCCA	TGACNAAGGC	TCC CTTCANG	TTAAATACNN	60
CCTAGNAAAC	ATTAATGGGT	TGCTCTACTA	ATACATCATA	CNAACCAGTA	AGCCTGCCA	120
NAACGCCAAC	TCAGGCCATT	CCTACCAAAG	GAAGAAAGGC	TGGTCTCTCC	ACCCCCTGTA	180
GGAAAGGCCT	GCCTTGTAAG	ACACCACAAT	NCGGCTGAAT	CTNAAGTCTT	GTGTTTACT	240
AATGGAAAAA	AAAAATAAAC	AANAGGTTT	GTTCTCATGG	CTGCCACCG	CAGCCTGGCA	300
CTAAAACANC	CCAGCGCTCA	CTTCTGCTTG	GANAAATATT	CTTGCTCTT	TTGGACATCA	360
GGCTTGATGG	TATCACTGCC	ACNTTTCCAC	CCAGCTGGGC	NCCCTTCCCC	CATNTTTGTC	420
ANTGANCTGG	AAGGCCTGAA	NCTTAGTCTC	CAAAAGTCTC	NGCCCACAAAG	ACCGGCCACC	480
AGGGGANGTC	NTTNCAGTG	GATCTGCCAA	ANANTACCCN	TATCATCNNT	GAATAAAAAG	540
GCCCCTGAAC	GANATGCTTC	CANCANCCTT	TAAGACCCAT	AATCCTNGAA	CCATGGTGCC	600
CTTCCGGTCT	GATCCNAAAG	GAATGTTCCCT	GGGTCCCANT	CCCTCCTTTG	TTNCTTACGT	660
TGTNTTGGAC	CCNTGCTNGN	ATNACCCAAN	TGANATCCCC	NGAAGCACCC	TNCCCTGGC	720
ATTTGANTTT	CNTAAATTCT	CTGCCCTACN	NCTGAAAGCA	CNATTCCCTN	GGCNCCNAAN	780
GGNGAACTCA	AGAAGGTCTN	NGAAAAACCA	CNCN			814

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCATGCTGCT	CTTCCTCAAA	GTTGTTCTTG	TTGCCATAAC	AACCACCATA	GGTAAAGCGG	60
GCGCAGTGTT	CGCTGAAGGG	GTTGTTAGTAC	CAGCGCGGG	TGCTCTCCTT	GCAGAGTCCT	120
GTGTCTGGCA	GGTCCACGCA	ATGCCCTTG	TCACTGGGA	AATGGATGCG	CTGGAGCTCG	180
TCNAANCCAC	TCGTGTATT	TTCACANGCA	GCCTCCTCCG	AAGCNTCCGG	GCAGTTGGGG	240
GTGTCGTAC	ACTCCACTAA	ACTGTCGATN	CANCAAGCCA	TTGCTGCAGC	GGAACTGGGT	300
GGGCTGACAG	GTGCCAGAAC	ACACTGGATN	GGCCTTCCA	TGGAAGGGCC	TGGGGAAAT	360
CNCCTNANCC	CAAAC TGCT	CTCAAAGGCC	ACCTTGACACA	CCCCGACAGG	CTAGAAATGC	420
ACTCTTCTTC	CCAAAGGTAG	TTGTTCTTGT	TGCCCAAGCA	NCCTCCANCA	AACCAAAANC	480
TTGCAAAATC	TGCTCCGTGG	GGGTCACTNNN	TACCANGTT	GGGGAAANAA	ACCCGGCNGN	540
GANCCNCCTT	GTGGAATGC	NAAGGNAATA	ATCCTCCTGT	CTTGCTTGGG	TGGAANAGCA	600
CAATTGAACT	GTAAACNTTG	GGCCGNGTTC	CNCTNGGGTG	GTCTGAAACT	AATCACCGTC	660
ACTGGAAAAA	GGTANGTGCC	TTCCTTGAAT	TCCCAAANTT	CCCCTNGNTT	TGGGTNNTTT	720
CTCCTCTNCC	CTAAAAATCG	TNTTCCCCCC	CCNTANGGCG			760

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTAAAAAA	CCCCCTCCAT	TGAATGAAAA	60
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CTTCCNAAAT	TGTCCAACCC	CCTCNNCAA	ATNNCCATT	CCGGGGGGGG	GTTCAAACC	120
CAAATTAATT	TTGGANTTTA	AATTAAATNT	TNATTNGGGG	AANAANCAA	ATGTNAAGAA	180
AATTTAACCC	ATTATNAACT	TAAATNCCTN	GAAACCCNTG	GNTCCAAAAA	ATTTTAACC	240
CTTAAATCCC	TCCGAAATTG	NTAANGAAA	ACCAAATTCTN	CCTAAGGCTN	TTTGAAGGTT	300
NGATTAAAC	CCCCTTNANT	TNTTTNACC	CNNGNCTNAA	NTATTTNGNT	TCCGGTGT	360
TCCTNTTAAN	CNTNGGTAAC	TCCCNGTAAT	GAANNNCCT	AANCCAATT	AACCGAATT	420
TTTTGAATT	GGAAATTCCN	NGGAATTNA	CCGGGGTTTT	TCCCNNTTGG	GGGCCATNCC	480
CCCNCTTCG	GGGTTGGGN	NTAGGTTGAA	TTTTNNANG	NCCCAAAAAA	NCCCCAANA	540
AAAAAACTCC	CAAGNNTTAA	TTNGAATNTC	CCCCCTCCCA	GGCCTTTGG	GAAAGGNGGG	600
TTTNTGGGG	CCNGGGANTT	CNTTCCCCCN	TTNCCNCCCC	CCCCCCNGGT	AAANGTTAT	660
NGNNTTGGT	TTTGGGCC	CTTNANGGAC	CTTCCGGATN	GAAATTAAAT	CCCCGGGNCG	720
					GCCG	724

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTTTTTTTT	TTTTCTTTG	CTCACATT	ATTTTATT	TGATTTTTT	TAATGCTGCA	60
CAACACAATA	TTTATTTCAT	TTGTTCTTT	TATTCATT	TATTTGTTG	CTGCTGCTGT	120
TTTATTATT	TTTACTGAAA	GTGAGAGGGA	ACTTTGTGG	CCTTTTTCC	TTTTCTGT	180
GGCCGCCTTA	AGCTTTCTAA	ATTTGGAACA	TCTAAGCAAG	CTGAANGGAA	AAGGGGGTTT	240
CGCAAAATCA	CTCGGGGAA	NGGAAAGGTT	GCTTGTTAA	TCATGCCCTA	TGGTGGGTGA	300
TTAACTGCTT	GTACAATTAC	NTTCACTTT	TAATTAATTG	TGCTNAANGC	TTTAATTANA	360
CTTGGGGGTT	CCCTCCCCAN	ACCAACCCN	CTGACAAAAA	GTGCCNGCCC	TCAAATNATG	420
TCCCAGCNNT	CNTTGAAACA	CACNGCNGAA	NGTTCTCATT	NTCCCCNCNC	CAGGTNAAAA	480
TGAAGGGTTA	CCATNTTTAA	CNCCACCTCC	ACNTGGCN	GCCTGAATCC	TCNAAAANCN	540
CCCTCAANCN	AATTNCTNNG	CCCCGGTCNC	GCNTNNGTCC	CNCCCAGGCT	CCGGGAANTN	600
CACCCCNNGA	ANNCNNTNNC	NAACNAAATT	CCGAAAATAT	TCCCNNTCNC	TCAATTCCCC	660
CNNAGACTNT	CCTCNANCN	CNCAATTTC	TTTTNNTCAC	GAACNCGNNC	CNAAAATGN	720
NNNNCNCTC	CNCTNGTCCN	NAATCNCCAN	C			751

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTGGTATT	CTGTAAGATC	AGGTGTCCT	CCCTCGTAGG	TTTAGAGGAA	ACACCCCTCAT	60
AGATGAAAAC	CCCCCCGAGA	CAGCAGCACT	GCAACTGCCA	AGCAGCCGGG	GTAGGAGGGG	120
CGCCCTATGC	ACAGCTGGGC	CCTTGAGACA	GCAGGGCTTC	GATGTCAGGC	TCGATGTCAA	180
TGGTCTGGAA	CGGGCGGCTG	TACCTGCGTA	GGGGCACACC	GTCAGGGCCC	ACCAGGAACT	240
TCTCAAAGTT	CCAGGCAACN	TCGTTGCGAC	ACACCGGAGA	CCAGGTGATN	AGCTTGGGGT	300
CGGTCTAACN	CGCGGTGGCG	TCGTCGCTGG	GAGCTGGCAG	GGCCTCCCGC	AGGAAGGCNA	360
ATAAAAGGTG	CGCCCCCGCA	CCGTTCANCT	CGCACTTCTC	NAANACCATG	ANGTTGGGCT	420

CNAACCCACC ACCANNCCGG ACTTCCTTGA NGGAATTCCC AAATCTCTTC GNTCTTGGC	480
TTCTNCTGAT GCCCTANCTG GTTGCCTCNGN ATGCCAANCA NCCCCAANCC CCGGGGTCCT	540
AAANCACCCN CCTCCTCNTT TCATCTGGGT TNTTNTCCCC GGACCNTGGT TCCTCTCAAG	600
GGANCCCATA TCTCNACCAN TACTCACCNT NCCCCCCCNT GNNACCCANC CTTCTANNGN	660
TTCCCNCCCG NCCTCTGGCC CNTCAAANAN GCTTNCACNA CCTGGGTCTG CCTTCCCCCC	720
TNCCCTATCT GNACCCNCN TTTGTCTCAN TNT	753

## (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 341 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACTATATCCA TCACAAACAGA CATGCTTCAT CCCATAGACT TCTTGACATA GCTTCAAATG	60
AGTGAACCCA TCCTTGATTT ATATACATAT ATGTTCTCAG TATTTTGGGA GCCTTTCCAC	120
TTCTTAAAC CTTGTTCAATT ATGAACACTG AAAATAGGAA TTTGTGAAGA GTAAAAAAGT	180
TATAGCTTGT TTACGTAGTA AGTTTTGAA GTCTACATTC AATCCAGACA CTTAGTTGAG	240
TGTTAAACTG TGATTTTAA AAAATATCAT TTGAGAATAT TCTTCAGAG GTATTTCAT	300
TTTTACTTTT TGATTAATTG TGTTTATAT ATTAGGGTAG T	341

## (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 101 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACTTACTGAA TTTAGTTCTG TGCTCTTCCT TATTAGTGT TGTATCATAA ATACTTTGAT	60
GTTTCAAACA TTCTAAATAA ATAATTTCA GTGGCTTCAT A	101

## (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACATCTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCTTCCTG GTCCTCACCC	60
TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTACAGC AAATTAAGAT	120
TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAGTCT AAGAAACCCA	180
CCTCTTGAGA GGTCAGTAAA GAGGACTTAA TATTCATAT CTACAAAATG ACCACAGGAT	240
TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC	300
TCGAA	305

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACATAAATAT CAGAGAAAAG TAGTCTTGA AATATTTACG TCCAGGAGTT CTTTGTCT 60	
GATTATTGG TGTGTGTTT GGTTGTGTC CAAAGTATTG GCAGCTTCAG TTTTCATTTC 120	
CTCTCCATCC TCGGGCATTTC TTCCCAAATT TATATACCAAG TCTTCGTCCA TCCACACGCT 180	
CCAGAATTTC TCTTTGTTAG TAATATCTCA TAGCTCGGCT GAGCTTTCA TAGGTCACTGC 240	
TGCTGTTGTT CTTCTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTC AAGAACCTGA 300	
AGACGCCCTC AGATCGGTCT TCCCATTAA TTAATCCTGG GTTCTTGCTCT GGGTTCAAGA 360	
GGATGTCGCG GATGAATTCC CATAAGTGAG TCCCTCTCGG GTTGTGCTTT TTGGTGTGGC 420	
ACTTGGCAGG GGGGTCTTGC TCCTTTTCA TATCAGGTGA CTCTGCAACA GGAAGGTGAC 480	
TGGTGGTTGT CATGGAGATC TGAGCCCGGC AGAAAGTTT GCTGTCCAAC AAATCTACTG 540	
TGCTACCATA GTTGGTGTCA TATAAATAGT TCTNGTCTT CCAGGTGTTC ATGATGGAAG 600	
GCTCAGTTG TTCAGTCTTG ACAATGACAT TGTGTGTGGA CTGGAACAGG TCACTACTGC 660	
ACTGGCCGTT CCACTTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCG GCCGTCCCTG 720	
CCGCCCGGGT GAACTCCTGC AAACATCATGC TGCAAAGGTG CTCGCCGTG ATGTCGAACT 780	
CNTGGAAAGG GATACAATTG GCATCCAGCT GGTTGGTGTCA CAGGAGGTGA TGGAGCCACT 840	
CCCACACCTG GT	852

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG	60
--------------------------------------------------------------------	----

AGTCTGACAC CATCCGGAGC ATCAGCATTG CTTCGCAGTG CCCTACCGCG GGGAACTCTT	120
GCCTCGTTTC TGGCTGGGCT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCAGTGCG	180
TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT	234

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTTATT TAAATGTTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA	60
ATTTGATAGC AATATTTGG AGATTACAGA GTTTAGTAA TTACCAATTAA CACAGTTAAA	120
AAGAAGATAA TATATTCCAA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAAA	180
TGANTATAAC TAATTGACAA TGGAAAATCA ATTTAATGT GAATTGCACA TTATCCTTTA	240
AAAGCTTCA AAANAAAANAA TTATTGCACT CTANTTAATT CAAACAGTGT TAAATGGTAT	300
CAGGATAAAAN AACTGAAGGG CANAAAGAAT TAATTTCAC TTCATGTAAC NCACCCANAT	360
TTACAATGGC TTAAATGCAN GGAAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTTC	420
TGGTCTCTAA TCTGCCTTAC TCTTGGGTG TGGCTTGAT CCTCTGGAGA CAGCTGCCAG	480
GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAG GACACATGCT	540
GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT	590

## (2) INFORMATION FOR SEQ ID NO:47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTAAAG AAGGAAAAAA AACGAGGCC	60
TGAACAGAAT TTTCCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGA GTTCAAGAC	120
GCTTCACTGC TTGAAACTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG	180
CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAG GGGACAAAGG CTAATCCAA	240
AACATCAAAG AAAGGAAGGT GGCGTCATAC CTCCCAGCCT ACACAGTTCT CCAGGGCTCT	300
CCTCATCCCT GGAGGACGAC AGTGGAGGAA CAACTGACCA TGTCAGGAGG CTCCTGTGTG	360
CTGGCTCCTG GTCTTCAGCC CCCAGCTCTG GAAGCCCACC CTCTGCTGAT CCTGCGTGGC	420
CCACACTCCT TGAACACACA TCCCCAGGTT ATATTCTGG ACATGGCTGA ACCTCCTATT	480
CCTACTTCCG AGATGCCTTG CTCCCTGCAG CCTGTAAAAA TCCCACTCAC CCTCCAAACC	540
ACGGCATGGG AAGCCTTCT GACTTGCTG ATTACTCCAG CATCTGGAA CAATCCCTGA	600
TTCCCCACTC CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC	660
AGGCTGCTGG CTTCAAATTN TGGCTCATT ACAGAGCTATG GGACCTTGGGG CAAGTNATCT	720
TCACTTCTAT GGGCNTCATT TTGTTCTACC TGCAAAATGG GGGATAATAA TAGT	774

## (2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CANAAAATTGA AATTTTATAA AAAGGCATT TTCTCTTATA TCCATAAAAT GATATAATT	60
TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTTCCCTT AATTACAGCT CAACGCAACT	120
TGGT	124

## (2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCGATGCTA CTATTTATT GCAGGAGGTG GGGGTGTTT TATTATTCTC TCAACAGCTT	60
TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTT TACGGGTGAT TGCAAAAATT	120
TTAGGGCACC CATATCCCAA GCANTGT	147

## (2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACATTAATT AATAAAAGGA CTGTTGGGT TCTGCTAAA CACATGGCTT GATATATTGC	60
ATGGTTTGAG GTTAGGAGGA GTTAGGCATA TGTTTGGGA GAGGGGT	107

## (2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCCTAGGAA	GTCTAGGGAA	CACACGACTC	TGGGGTCACG	GGGCCGACAC	ACTTGCACGG	60
CGGGAAGGAA	AGGCAGAGAA	GTGACACCGT	CAGGGGGAAA	TGACAGAAAG	GAAAATCAAG	120
GCCTTGCAAG	GTCAGAAAGG	GGACTCAGGG	CTTCCACCAC	AGCCCTGCC	CACTTGGCCA	180
CCTCCCTTTT	GGGACCAGCA	ATGT				204

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAAAGATAA	CATTTATCTT	ATAACAAAAA	TTTGATAGTT	TTAAAGGTTA	GTATTGTGTA	60
GGGTATTTTC	CAAAAGACTA	AAGAGATAAC	TCAGGTAAAA	AGTTAGAAAT	GTATAAAACA	120
CCATCAGACA	GGTTTTTAAA	AAACAACATA	TTACAAAATT	AGACAATCAT	CCTTAAAAAA	180
AAAACTTCTT	GTATCAATT	CTTTGTTCA	AAATGACTGA	CTTAANTATT	TTTAAATATT	240
TCANAAACAC	TTCCTCAAAA	ATTTCAANA	TGGTAGCTT	CANATGTNCC	CTCAGTCCCA	300
ATGTTGCTCA	GATAAATAAA	TCTCGTGAGA	ACTTACCACC	CACCACAAGC	TTTCTGGGGC	360
ATGCAACAGT	GTCTTTCTT	TNCTTTTCT	TTTTTTTTT	TTACAGGCAC	AGAAACTCAT	420
CAATTTATT	TGGATAACAA	AGGGTCTCCA	AATTATATTG	AAAAATAAAT	CCAAGTTAAT	480
ATCACTCTG	T					491

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACATAATTAA	GCAGGGCTAA	TTACCATAAG	ATGCTATTAA	TTAANAGGTN	TATGATCTGA	60
GTATTAACAG	TTGCTGAAGT	TTGGTATTAA	TATGCAGCAT	TTTCTTTTG	CTTGATAAAC	120
ACTACAGAAC	CCTTAAGGAC	ACTGAAAATT	AGTAAGTAAA	GTTCAGAAAC	ATTAGCTGCT	180
CAATCAAATC	TCTACATAAC	ACTATAGTAA	TTAAAACGTT	AAAAAAAAGT	GTTGAAATCT	240
GCACTAGTAT	ANACCGCTCC	TGTCAAGGATA	ANACTGCTTT	GGAACAGAAA	GGGAAAAANC	300
AGCTTTGANT	TTCTTTGTGC	TGATANGAGG	AAAGGCTGAA	TTACCTTGT	GCCTCTCCCT	360
AATGATTGGC	AGGTCNGGTA	AATNCCAAAA	CATATTCCAA	CTCAACACTT	CTTTCCNCG	420
TANCTTGANT	CTGTGTATTTC	CAGGANCAGG	CGGATGGAAT	GGGCCAGCCC	NCGGATGTT	480
CANT						484

## (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 151 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACTAAACCTC	GTGCTTGTGA	ACTCCATACA	GAAAACGGTG	CCATCCCTGA	ACACGGCTGG	60
CCACTGGGTA	TACTGCTGAC	AACCGCAACA	ACAAAAAACAC	AAATCCTTGG	CACTGGCTAG	120
TCTATGTCCT	CTCAAGTGCC	TTTTGTTTG	T			151

## (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 91 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACCTGGCTTG	TCTCCGGGTG	GTTCCCGGCG	CCCCCCACGG	TCCCCAGAAC	GGACACTTTC	60
GCCCTCCAGT	GGATACTCGA	GCCAAAGTGG	T			91

## (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 133 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGGATGTG CGTTGGTTAT ATACAAATAT GTCATTTAT GTAAGGGACT TGAGTATACT	60
TGGATTTTG GTATCTGTGG GTTGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC	120
AAGGGACAAC TGT	133

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC	60
GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA	120
TCTCANTGGG CTGGATNCAT GCAGGGT	147

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGAAAATAC ATTGAATTCTT CTGTATACTC	60
TGATTACATA CATTATCCT TTAAAAAAGA TGTAATCTT AATTTTATG CCATCTATTA	120
ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TTAACTAGTT	180
TTGACTTCTA AGTTTGGT	198

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAAACAAATG GGTTGTGAGG AAGTCTTATC AGCAAAACTG GTGATGGCTA CTGAAAAGAT	60
CCATTGAAAA TTATCATTAA TGATTTAAA TGACAAGTTA TCAAAAACTC ACTCAATTTC	120
CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATACT ATCTTCTGAA	180
TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG	240
CAGAAGGAAT CTATTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT	300
TTTCGTCTTT ATTGGACTTC TTTGAAGAGT	330

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC	60
GTCGTGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCAC	120
TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGC ATTCCCGTGC CTGGT	175

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT	60
GGTTGTTGCT CTTCAACAGT ATCCTCCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC	120
TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT	154

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCTCGAGCC CTATAGTGAG TCGTATTAGA

30

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 89 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACAAGTCATT TCAGCACCCCT TTGCTCTTCA AAACTGACCA TCTTTATAT TTAATGCTTC  
CTGTATGAAT AAAAATGGTT ATGTCAAGT

60  
89

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 97 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCTGCAG  
AATCAGTGCA TCCAGGATTG GTCCTTGGAT CTGGGGT

60  
97

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 377 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ACAAACAANAA	NTCCCTTCTT	TAGGCCACTG	ATGGAAACCT	GGAACCCCT	TTTGATGGCA	60
GCATGGCGTC	CTAGGCCTTG	ACACAGCGGC	TGGGGTTTGG	GCTNTCCAA	ACCGCACACC	120
CCAACCCTGG	TCTACCCACA	NTTCTGGCTA	TGGGCTGTCT	CTGCCACTGA	ACATCAGGGT	180
TCGGTCATAA	NATGAAATCC	CAANGGGAC	AGAGGTCAGT	AGAGGAAGCT	CAATGAGAAA	240
GGTGCTGTT	GCTCAGCCAG	AAAACAGCTG	CCTGGCATTG	GCCGCTGAAC	TATGAACCCG	300
TGGGGGTGAA	CTACCCCCAN	GAGGAATCAT	GCCTGGCGA	TGCAANGGTG	CCAACAGGAG	360
GGGCGGGAGG	AGCATGT					377

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACGCCTTTCC	CTCAGAATT	AGGGAAAGAGA	CTGTCGCCTG	CCTTCCTCCG	TTGTTGCGTG	60
AGAACCCGTG	TGCCCTTCC	CACCATATCC	ACCCTCGCTC	CATCTTGAA	CTCAAACACG	120
AGGAACTAAC	TGCACCCCTGG	TCCTCTCCCC	AGTCCCCAGT	TCACCCCTCCA	TCCCTCACCT	180
TCCTCCACTC	TAAGGGATAT	CAACACTGCC	CAGCACAGGG	GCCCTGAATT	TATGTGGTTT	240
TTATATATTT	TTAATAAGA	TGCACTTAT	GTCATTTTT	AATAAAGTCT	GAAGAATTAC	300
TGTTT						305

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACTACACACA	CTCCACTTGC	CCTTGTGAGA	CACTTTGTCC	CAGCACTTTA	GGAATGCTGA	60
GGTCGGACCA	GCCACATCTC	ATGTGCAAGA	TTGCCAGCA	GACATCAGGT	CTGAGAGTTC	120
CCCTTTAAA	AAAGGGACT	TGCTTAAAAAA	AGAAGTCTAG	CCACGATTGT	GTAGAGCAGC	180
TGTGCTGTGC	TGGAGATTCA	CTTTGAGAG	AGTTCTCCTC	TGAGACCTGA	TCTTAGAGGG	240
CTGGGCAGTC	TTGCACATGA	GATGGGGCTG	GTCTGATCTC	AGCACTCCTT	AGTCTGCTTG	300
CCTCTCCCAG	GGCCCCAGCC	TGGCCACACC	TGCTTACAGG	GCACTCTCAG	ATGCCCATAC	360
CATAGTTCT	GTGCTAGTGG	ACCGT				385

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACTTAACCAG ATATATTTT ACCCCAGATG GGGATATTCT TTGTAAAAAA TGAAAATAAA	60
GTTTTTTAA TGG	73

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 536 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGGGCTC TCACCCTCCT CTCCTGCAGC	60
TCCAGCTTTG TGCTCTGCCT CTGAGGAGAC CATGGCCAG CATCTGAGTA CCCTGCTGCT	120
CCTGCTGGCC ACCCTAGCTG TGGCCCTGGC CTGGAGCCCC AAGGAGGAGG ATAGGATAAT	180
CCCGGGTGGC ATCTATAACG CAGACCTCAA TGATGAGTGG GTACAGCGTG CCCTTCACCT	240
CGCCATCAGC GAGTATAACA AGGCCACCAA AGATGACTAC TACAGACGTC CGCTGCGGGT	300
ACTAAGAGCC AGGCAACAGA CCGTTGGGG GGTGAATTAC TTCTTCGACG TAGAGGTGGG	360
CCGAACCATA TGTACCAAGT CCCAGCCCAA CTTGGACACC TGTGCCTTCC ATGAACAGCC	420
AGAACTGCAG AAGAAACAGT TGTGCTCTTT CGAGATCTAC GAAGTTCCCT GGGGAGAACAA	480
GAANGTCCCT GGGTGAAATC CAGGTGTCAA GAAATCCTAN GGATCTGTTG CCAGGC	536

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 477 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGACCCCTA ACAGGGGCCCT TCTCAGCCCT CCTAATGACC TCCGGCCTAG CCATGTGATT	60
TCACTTCCAC TCCATAACGC TCCTCATACT AGGCCTACTA ACCAACACAC TAACCATATA	120
CCAATGATGG CGCGATGTAA CACGAGAAAG CACATACCAA GGCCACCACA CACCACCTGT	180

CCAAAAAGGC CTTCGATACG GGATAATCCT ATTATTACC TCAGAAGTTT TTTTCTTCGC	240
AGGGATTTT CTGAGCCTT TACCACTCCA GCCTAGCCCC TACCCCCCAA CTAGGAGGGC	300
ACTGGCCCCC AACAGGCATC ACCCCGCTAA ATCCCCTAGA AGTCCCACTC CTAAACACAT	360
CCGTATTACT CGCATCAGGA GTATCAATCA CCTGAGCTCA CCATAGTCTA ATAGAAAACA	420
ACCGAAACCA AATTATTCAA AGCACTGCTT ATTACAATT TACTGGGTCT CTATTTT	477

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 533 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGAGCTATAG GTACAGTGTG ATCTCAGCTT TGCAAACACA TTTTCTACAT AGATAGTACT	60
AGGTATTAAT AGATATGTAA AGAAAGAAAT CACACCATTAA ATAATGGTAA GATTGGTTA	120
TGTGATTTA GTGGTATTCTT TGGCACCCCTT ATATATGTTT TCCAAACTTT CAGCAGTGAT	180
ATTATTCCA TAACTAAAAA AGTGAGTTTG AAAAAGAAAA TCTCCAGCAA GCATCTCATT	240
TAAATAAAGG TTTGTCATCT TTAAAAATAC AGCAATATGT GACTTTTAA AAAAGCTGTC	300
AAATAGGTGT GACCCTACTA ATAATTATTA GAAATACATT TAAAAACATC GAGTACCTCA	360
AGTCAGTTTG CCTTGAAAAA TATCAAATAT AACTCTTAGA GAAATGTACA TAAAAGAATG	420
CTTCGTAATT TTGGAGTANG AGGTTCCCTC CTCAATTGGT TATTTTAAA AAGTACATGG	480
TAAAAAAA AATTACAAC AGTATATAAG GCTGTAAAAT GAAGAATTCT GCC	533

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 511 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TATTACGGAA AAACACACCA CATAATTCAA CTANCAAAGA ANACTGCTTC AGGGCGTGTAA	60
AAATGAAAGG CTTCCAGGCA GTTATCTGAT TAAAGAACAC TAAAAGAGGG ACAAGGCTAA	120
AAGCCGCAGG ATGTCTACAC TATANCAGGC GCTATTGGG TTGGCTGGAG GAGCTGTGGA	180
AAACATGGAN AGATTGGTGC TGGANATCGC CGTGGCTATT CCTCATTGTT ATTACANAGT	240
GAGGTTCTCT GTGTGCCAC TGGTTGAAA ACCGTTCTNC AATAATGATA GAATAGTACA	300
CACATGAGAA CTGAAATGGC CCAAACCCAG AAAGAAAGCC CAACTAGATC CTCAGAANAC	360
GCTTCTAGGG ACAATAACCG ATGAAGAAAA GATGGCCTCC TTGTGCCCCC GTCTGTTATG	420
ATTTCCTCTCC ATTGCAGCNA NAAACCCGTT CTTCTAAGCA AACNCAGGTG ATGATGGCNA	480
AAATACACCC CCTCTTGAAG NACCNGGAGG A	511

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAGTGCCAGC	ACTGGTGCCA	GTACCA	GTCAGTAC	CAATAACAGT	GCCAGTGCCA	GTGCCAGCAC	60
CAGTGGTGGC	TTCAGTGCTG	GTGCCAGCCT	GACCGCCACT	CTCACATTG	GGCTCTTCGC		120
TGGCCTTGGT	GGAGCTGGTG	CCAGCACCAAG	TGGCAGCTCT	GGTGCCTGTG	GTTTCTCCTA		180
CAAGTGAGAT	TTTAGATATT	GTAAATCCTG	CCAGTCTTC	TCTTCAAGCC	AGGGTGCATC		240
CTCAGAAACC	TACTCAACAC	AGCACTCTAG	GCAGCCACTA	TCAATCAATT	GAAGTTGACA		300
CTCTGCATTA	AATCTATTG	CCATTCTGA	AAAAAAAAAA	AAAAAAAGGG	CGGCCGCTCG		360
ANTCTAGAGG	GCCCCTTAA	ACCCGCTGAT	CAGCCTCGAC	TGTGCCTTCT	ANTGCCAGC		420
CATCTGTTGT	TTGCCCTCCTCC	CCCGNTGCCT	TCCTTGACCC	TGGAAAGTGC	CACTCCCAC		480
GTCCTTCCT	AANTAAAAT						499

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTTCATAGGA	GAACACACTG	AGGAGATACT	TGAAGAATT	GGATTCA	GCGAAGAGAT	60
TTATCAGCTT	AACTCAGATA	AAATCATTGA	AAGTAATAAG	GTAAAAGCTA	GTCTCTAACT	120
TCCAGGCCA	CGGCTCAAGT	GAATTGAA	ACTGCATT	CAGTGTAGAG	TAACACATAA	180
CATTGTATGC	ATGGAAACAT	GGAGGAACAG	TATTACAGT	TCCTACCACT	CTAATCAAGA	240
AAAGAATTAC	AGACTCTGAT	TCTACAGTGA	TGATTGAATT	CTAAAAATGG	TAATCATTAG	300
GGCTTTGAT	TTATAANACT	TTGGGTACTT	ATACTAAATT	ATGGTAGTTA	TACTGCCTTC	360
CAGTTGCTT	GATATATTG	TTGATATTAA	GATTCTGAC	TTATATTG	AATGGGTTCT	420
ACTGAAAAN	GAATGATATA	TTCTTGAAGA	CATCGATATA	CATTATT	CACTCTTGAT	480
TCTACAATGT	AGAAAATGAA	GGAAATGCC	CAAATTGTAT	GGTGATAAAA	GTCCCGT	537

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAAANACAAT	TGTTCAAAAG	ATGCAAATGA	TACACTACTG	CTGCAGCTCA	CAAACACCTC	60
TGCATATTAC	ACGTACCTCC	TCCTGCTCCT	CAAGTAGTGT	GGTCTATTT	GCCATCATCA	120
CCTGCTGTCT	GCTTAGAAGA	ACGGCTTCT	GCTGCAANGG	AGAGAAATCA	TAACAGACGG	180
TGGCACAAAGG	AGGCCATCTT	TTCCTCATCG	GTTATTGTCC	CTAGAAGCGT	CTTCTGAGGA	240
TCTAGTTGGG	CTTTCTTCT	GGGTTTGGGC	CATTCANTT	CTCATGTGTG	TACTATTCTA	300
TCATTATTGT	ATAACGGTTT	TCAAACCNGT	GGGCACNCAG	AGAACCTCAC	TCTGTAATAA	360
CAATGAGGAA	TAGCCACGGT	GATCTCCAGC	ACCAAATCTC	TCCATGTTNT	TCCAGAGCTC	420
CTCCAGCCAA	CCCAAATAGC	CGCTGCTATN	GTGTAGAAC	TCCCTGN		467

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGCTGACAG	CATTGGGCC	GAGATGTCTC	GCTCCGTGGC	CTTAGCTGTG	CTCGCGCTAC	60
TCTCTCTTTC	TGGCCTGGAG	GCTATCCAGC	GTACTCCAAA	GATTCAAGTT	TACTCACGTC	120
ATCCAGCAGA	GAATGGAAAG	TCAAATTCC	TGAATTGCTA	TGTGTCTGGG	TTTCATCCAT	180
CCGACATTGA	AGTTGACTTA	CTGAAGAATG	GAGAGAGAAT	TGAAAAAAGTG	GAGCATTCAAG	240
ACTTGTCTTT	CAGCAAGGAC	TGGTCTTCT	ATCTCTTGTA	CTACACTGAA	TTCACCCCCA	300
CTGAAAAAGA	TGAGTATGCC	TGCCGTGTGA	ACCATGTGAC	TTTGTACAG	CCCAAGATNG	360
TTNAGTGGGA	TCGANACATG	TAAGCAGCAN	CATGGGAGGT			400

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGGAGTGCC	TTGGTGTTC	AAGCCCTGC	AGGAAGCAGA	ATGCACCTTC	TGAGGCACCT	60
CCAGCTGCC	CGGCGGGGGA	TGCGAGGCTC	GGAGCACCC	TGCCCCGGCTG	TGATTGCTGC	120
CAGGCACTGT	TCATCTCAGC	TTTTCTGTCC	CTTTGCTCCC	GGCAAGCGCT	TCTGCTGAAA	180
GTTCATATCT	GGAGCCTGAT	GTCTAACGA	ATAAAGGTCC	CATGCTCCAC	CCGAAAAAAA	240
					AAAAAAA	248

## (2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCAA CACAATGGCT ACCTTTAACA	60
TCACCCAGAC CCCGCCCTGC CGCTGCCCA CGCTGCTGCT AACGACAGTA TGATGCTTAC	120
TCTGCTACTC GGAAACTATT TTTATGTAAT TAATGTATGC TTTCTTGTTC ATAAATGCCT	180
GATTTAAAAA AAAAAAAA A	201

## (2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCTTTGTT AGGTTTTGA GACAACCCTA GACCTAAACT GTGTCACAGA CTTCTGAATG	60
TTTAGGCAGT GCTAGTAATT TCCTCGTAAT GATTCTGTTA TTACTTTCCCT ATTCTTTATT	120
CCTCTTCCTT CTGAAGATTA ATGAAGTTGA AAATTGAGGT GGATAAATAC AAAAAGGTAG	180
TGTGATAGTA TAAGTATCTA AGTGCAGATG AAAGTGTGTT ATATATATCC ATTCAAAATT	240
ATGCAAGTTA GTAATTACTC AGGGTTAACT AAATTACTTT AATATGCTGT TGAACCTACT	300
CTGTTCCCTG GCTAGAAAAA ATTATAAACCA GGACTTTGTT AGTTGGGAA GCCAAATTGA	360
TAATATTCTA TGTTCTAAA GTTGGGCTAT ACATAAANTA TNAAGAAATA TGGAATTTTA	420
TTCCCAAGGAA TATGGGGTTC ATTTATGAAT ANTACCCGGG ANAGAAGTTT TGANTNAAAC	480
CNGTTTGTT TAATACGTTA ATATGTCCTN AATNAACAAG GCNTGACTTA TTTCCAAAAAA	540
AAAAAAA A	552

## (2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATT	GAGATGCTAA	GGCCCCAGAG	ATCGTTGAT	CCAACCCTCT	TATTTTCAGA	60
GGGGAAAATG	GGGCCTAGAA	GTTACAGAGC	ATCTAGCTGG	TGCGCTGGCA	CCCCTGGCCT	120
CACACAGACT	CCCGAGTAGC	TGGGACTACA	GGCACACAGT	CACTGAAGCA	GGCCCTGTTT	180
GCAATTACAG	TTGCCACCTC	CAACTTAAAC	ATTCTTCATA	TGTGATGTCC	TTAGTCACTA	240
AGGTTAAACT	TTCCCACCCA	GAAAAGGCAA	CTTAGATAAA	ATCTTAGAGT	ACTTTCATAC	300
TCTTCTAAGT	CCTCTTCCAG	CCTCACTTTG	AGTCCTCCTT	GGGGGTTGAT	AGGAANTNTC	360
TCTTGGCTTT	CTCAATAAAA	TCTCTATCCA	TCTCATGTTT	AATTTGGTAC	GCNTAAAAAT	420
GCTGAAAAAA	TTAAAATGTT	CTGGTTTCNC	TTTAAAAAAA	AAAAAAA	AAAAAA	476

## (2) INFORMATION FOR SEQ ID NO:81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTTG	TATGCCNTCN	CTGTGGNGTT	ATTGTTGCTG	CCACCCTGGA	GGAGCCCAGT	60
TTCTTCTGTA	TCTTTCTTTT	CTGGGGGATC	TTCCTGGCTC	TGCCCCTCCA	TTCCCAGCCT	120
CTCATCCCCA	TCTTGCACTT	TTGCTAGGGT	TGGAGGGCGCT	TTCCCTGGTAG	CCCCTCAGAG	180
ACTCAGTCAG	CGGGAATAAG	TCCTAGGGT	GGGGGGTGTG	GCAAGCCGGC	CT	232

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGGCGGGAGC	AGAAGCTAAA	GCCAAAGCCC	AAGAAGAGTG	GCAGTGCCAG	CACTGGTGCC	60
AGTACCAGTA	CCAATAACAT	GCCAGTGCCA	GTGCCAGCAC	CAGTGGTGGC	TTCAGTGCTG	120
GTGCCAGCCT	GACCGCCACT	CTCACATTG	GGCTCTTCGC	TGGCCTTGGT	GGAGCTGGTG	180
CCAGCACCAAG	TGGCAGCTCT	GGTGCCTGTG	GTTTCTCCTA	CAAGTGAGAT	TTTAGATATT	240
GTAAATCCTG	CCAGTCTTTC	TCTTCAAGCC	AGGGTGCATC	CTCAGAAACC	TACTCAACAC	300
AGCACTCTNG	GCAGCCACTA	TCAATCAATT	GAAGTTGACA	CTCTGCATTA	AATCTATTG	360
CCATTCAAA	AAAAAAA	AAA				383

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCCTC CAGTATTACC TCAACGAGCA	60
GGGAGATCGA GTCTATACGC TGAAGAAATT TGACCCGATG GGACAACAGA CCTGCTCAGC	120
CCATCCTGCT CGGTTCTCCC CAGATGACAA ATACTCTCGA CACCGAATCA CCATCAAGAA	180
ACGCTTCAAG GTGCTCATGA CCCAGCAACC GCGCCCTGTC CTCTGAGGGT CCTTAAACTG	240
ATGTCTTTTC TGCCACCTGT TACCCCTCGG AGACTCCGTA ACCAAACTCT TCGGACTGTG	300
AGCCCTGATG CCTTTTGCC AGCCATACTC TTTGGCNTCC AGTCTCTCGT GGCAGATTGAT	360
TATGCTTGTG TGAGGCAATC ATGGTGGCAT CACCCATNAA GGGAACACAT TTGANTTTT	420
TTTCNCATAT TTTAAATTAC NACCAGAATA NTTCAGAATA AATGAATTGA AAAACTCTTA	480
AAAAAAAAAAA AAAA	494

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 380 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTGGTAGCC TATGGCGTGG CCACGGANGG GCTCCTGAGG CACGGGACAG TGACTTCCA	60
AGTATCCTGC GCCGCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGGCA GATTCCCCAG	120
GAGGACATGG ACGTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG	180
GCACACCCTC CTGGGGCCCA GGCGGGCACC TGCGTCTCCC AGTATGCCAA CTGGCTGGTG	240
GTGCTGCTCC TCGTCATCTT CCTGCTCGTG GCCAACATCC TGCTGGTCAC TTGCTCATTG	300
CCATGTTCAAG TTACACATTC GGCAAAGTAC AGGGCAACAG CNATCTCTAC TGGGAAGGCC	360
AGCGTTNCCG CCTCATCCGG	380

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 481 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAGTTAGCTC	CTCCACAACC	TTGATGAGGT	CGCTCTGAGT	GGCCTCTCGC	TTCATACCGC	60
TNCCATCGTC	ATACTGTAGG	TTTGCCACCA	CCTCCTGCAT	CTTGGGGCGG	CTAATATCCA	120
GGAAACTCTC	AATCAAGTCA	CCGTCNATNA	AACCTGTGGC	TGGTTCTGTC	TTCCGCTCGG	180
TGTGAAAGGA	TCTCCAGAAG	GAGTGTCTGA	TCTTCCCCAC	ACTTTGATG	ACTTTATTGA	240
GTCGATTCTG	CATGTCCAGC	AGGAGGTTGT	ACCAAGCTCTC	TGACAGTGAG	GTCACCAGCC	300
CTATCATGCC	NTTGAACGTG	CCGAAGAACCA	CCGAGCCTTG	TGTGGGGGGT	GNAGTCTCAC	360
CCAGATTCTG	CATTACCAAGA	NAGCCGTGGC	AAAAGANATT	GACAACCTCGC	CCAGGNNGAA	420
AAAGAACACC	TCCTGGAAAGT	GCTNGCCGCT	CCTCGTCCNT	TGGTGGNNNGC	GCNTNCCTTT	480
T						481

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TTGTCTGCTG	AGAATTCAATT	60
ACTTGGAAAA	GCAACTTNA	GCCTGGACAC	TGGTATTAAA	ATTCAACAATA	TGCAACACTT	120
TAAACAGTGT	GTCAATCTGC	TCCCTTACTT	TGTCATCACC	AGTCTGGAA	TAAGGGTATG	180
CCCTATTACAC	ACCTGTTAAA	AGGGCGCTAA	GCATTTTGA	TTCAACATCT	TTTTTTTGA	240
CACAAGTCCG	AAAAAAGCAA	AAGTAAACAG	TTNTTAATT	GTTAGCCAAT	TCACTTCTT	300
CATGGGACAG	AGCCATTGA	TTTAAAAGC	AAATTGCATA	ATATTGAGCT	TTGGGAGCTG	360
ATATNTGAGC	GGAAGANTAG	CCTTCTACT	TCACCAGACA	CAACTCCTT	CATATTGGGA	420
TGTTNACNA	AGTTATGTCT	CTTACAGATG	GGATGCTTT	GTGGCAATT	TG	472

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGAAACCAGT	ATCTCTNAAA	ACAACCTCTC	ATACCTTGTG	GACCTAATT	TGTGTGCGTG	60
TGTGTGTGCG	CGCATATTAT	ATAGACAGGC	ACATCTTTT	TACTTTGTA	AAAGCTTATG	120
CCTCTTGGT	ATCTATATCT	GTGAAAGTT	TAATGATCTG	CCATAATGTC	TTGGGGACCT	180
TTGTCTTCTG	TGTAAATGGT	ACTAGAGAAA	ACACCTATNT	TATGAGTCAA	TCTAGTTNGT	240
TTTATTCGAC	ATGAAGGAAA	TTTCCAGATN	ACAACACTNA	CAAACCTCTCC	CTTGACTAGG	300
GGGGACAAAG	AAAAGCANAA	CTGAACATNA	GAAACAATTN	CCTGGTGAGA	AATTNCATAAA	360
ACAGAAATTG	GGTNGTATAT	TGAAANANNG	CATCATTNA	ACGTTTTTT	TTT	413

## (2) INFORMATION FOR SEQ ID NO:88:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGCAGCGGGT	CCTCTCTATC	TAGCTCCAGC	CTCTCGCCTG	CCCCACTCCC	CGCGTCCCGC	60
GTCCTAGCCN	ACCATGGCCG	GGCCCCTGCG	CGCCCCGCTG	CTCCTGCTGG	CCATCCTGGC	120
CGTGGCCCTG	GCCGTGAGCC	CCGGGGCCGG	CTCCAGTCCC	GGCAAGCCGC	CGCGCCTGGT	180
GGGAGGCCCA	TGGACCCCGC	GTGGAAGAAG	AAGGTGTGCG	GCGTGCACTG	GACTTTGCCG	240
TCGGCNANTA	CAACAAACCC	GCAACNACTT	TTACCNAGCN	CGCGCTGCAG	GTGTTGCCGC	300
CCCAANCAAA	TTGTTACTNG	GGGTAANTAA	TTCTTGGAAAG	TTGAACCTGG	GCCAAACNNG	360
TTTACCAGAA	CCNAGCCAAT	TNGAACAAATT	NCCCTCCAT	AACAGCCCC	TTTAAAAAGG	420
GAANCANTCC	TGNTCTTTTC	CAAATTTT				448

## (2) INFORMATION FOR SEQ ID NO:89:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTTGTG	CACTGGCAC	TGTGATGGAA	CCATTGGGCC	AGGATGCTT	GAGTTTATCA	60
GTAGTGATT	TGCCAAAGTT	GGTGGTGTAA	CATGAGTATG	TAAAATGTCA	AAAAATTAGC	120
AGAGGTCTAG	GTCTGCATAT	CAGCAGACAG	TTTGTCCGTG	TATTTGTAG	CCTTGAAGTT	180
CTCAGTGACA	AGTTNNNTCT	GATGCGAAGT	TCTNATTCCA	GTGTTTAGT	CCTTGACATC	240
TTTNATGTTN	AGACTTGCCT	CTNTNAAATT	GCTTTGTNT	TCTGCAGGTA	CTATCTGTGG	300
TTTAACAAAA	TAGAANNACT	TCTCTGCTTN	GAANATTGA	ATATCTTACA	TCTNAAAATN	360
AATTCTCTCC	CCATANNAAA	ACCCANGCCC	TTGGGANAAT	TTGAAAANG	GNTCCTTCNN	420
AATTCCNNANA	ANTTCAGNTN	TCATACAACA	NAACNGGANC	CCC		463

## (2) INFORMATION FOR SEQ ID NO:90:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGGGATTGAA	GGTCTNTTNT	ACTGTCGGAC	TGTTCANCCA	CCAACTCTAC	AAGTTGCTGT	60
CTTCCACTCA	CTGCTCTGAA	GCNTNTAAC	CCAGACTGTA	TCTTCATAAA	TAGAACAAAT	120
TCTTCACCAG	TCACATCTTC	TAGGACCTT	TTGGATTCAAG	TTAGTATAAG	CTCTTCCACT	180
TCCTTTGTTA	AGACTTCATC	TGGTAAAGTC	TTAAGTTTG	TAGAAAGGAA	TTTAATTGCT	240
CGTTCTCTAA	CAATGTCTC	TCCTTGAAGT	ATTGGCTGA	ACAACCCACC	TNAAGTCCCT	300
TTGTGCATCC	ATTTAAATA	TACTTAATAG	GGCATTGGTN	CACTAGGTTA	AATTCTGCAA	360
GAGTCATCTG	TCTGCAAAAG	TTGCGTTAGT	ATATCTGCCA			400

## (2) INFORMATION FOR SEQ ID NO:91:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGCTCGGAT	CCAATAATCT	TTGCTTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCCTCTTT	GAECTACCGTG	TGCCAGTGCT	GGTGATTCTC	ACACACCTCC	NNCCGCTCTT	180
TGTGGAAAAAA	CTGGCACTTG	NCTGGAACTA	GCAAGACATC	ACTTACAAAT	TCACCCACGA	240
GACACTTGAA	AGGTGTAACA	AAGCGACTCT	TGCATTGCTT	TTTGTCCCTC	CGGCACCAAGT	300
TGTCAATACT	AACCCGCTGG	TTTGCCTCCA	TCACATTTGT	GATCTGTAGC	TCTGGATACA	360
TCTCCTGACA	GTACTGAAGA	ACTTCTTCTT	TTGTTTCAA	AGCAACTCTT	GGTGCCTGTT	420
NGATCAGGTT	CCCATTTCCC	AGTCCGAATG	TTACACATGGC	ATATNTTACT	TCCCACAAAA	480

## (2) INFORMATION FOR SEQ ID NO:92:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATACAGGCCA	NATCCCACCA	CGAAGATGCG	CTTGGTGA	GAGAACCTGA	TGCGGTC	60
GGTCCCGCTG	TAGCCCCAGC	GA	CTGCTGGAAG	CGGTTGATGC	TGCAC	120
CCCACGCAGG	CAGCAGCGGG	GGCGGTCAAT	GA	CGTGGCTTGG	GGTTGACGGT	180
TAANTGCAGG	AAGAGGCTGA	CCACCTCGCG	GTCCACCAGG	ATGCCCGACT	GTGCGGGACC	240

TGCAGCGAAA	CTCCTCGATG	GTCATGAGCG	GGAAGCGAAT	GANGCCCAGG	GCCTTGCCCA	300
GAACCTTCCG	CCTGTTCTCT	GGCGTCACCT	GCAGCTGCTG	CCGCTNACAC	TCGGCCTCGG	360
ACCAGCGGAC	AAACGGCGTT	GAACAGCCGC	ACCTCACGGA	TGCCCANTGT	GTCGCGCTCC	420
AGGAACGGCN	CCAGCGTGTC	CAGGTCAATG	TCGGTGAANC	CTCCGCGGGT	AATGGCG	477

## (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 377 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAACGGCTGG	ACCTTGCCTC	GCATTGTGCT	GCTGGCAGGA	ATACCTTGGC	AAGCAGCTCC	60
AGTCCGAGCA	GCCCCAGACC	GCTGCCGCC	GAAGCTAACG	CTGCCTCTGG	CCTTCCCCTC	120
CGCCTCAATG	CAGAACCA	AGTGGGAGCA	CTGTGTTAG	AGTTAAGAGT	GAACACTGTN	180
TGATTTTACT	TGGGAATTTC	CTCTGTTATA	TAGCTTTCC	CAATGCTAAT	TTCCAAACAA	240
CAACAAACAAA	ATAACATGTT	TGCCTGTTNA	GTTGTATAAA	AGTANGTGAT	TCTGTATNTA	300
AAGAAAATAT	TACTGTTACA	TATACTGCTT	GCAANTTCTG	TATTTATTGG	TNCTCTGGAA	360
ATAAATATAT	TATTA	AAA	AAA	AAA	AAA	377

## (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 495 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCCTTGAGG	GGTTAGGGTC	CAGTTCCCAG	TGGAAGAAC	AGGCCAGGAG	AANTGCGTGC	60
CGAGCTGANG	CAGATTCCC	ACAGTGACCC	CAGAGCCCTG	GGCTATAGTC	TCTGACCCCT	120
CCAAGGAAAG	ACCACCTTCT	GGGGACATGG	GCTGGAGGGC	AGGACCTAGA	GGCACCAAGG	180
GAAGGCCCA	TTCCGGGGCT	GTTCCCCGAG	GAGGAAGGGA	AGGGGCTCTG	TGTCCCCCCC	240
ACGAGGAANA	GGCCCTGANT	CCTGGGATCA	NACACCCCTT	CACGTGTATC	CCCACACAAA	300
TGCAAGCTCA	CCAAGGTCCC	CTCTCAGTCC	CTTCCCTACA	CCCTGAACGG	NCACTGGCCC	360
ACACCCACCC	AGANCANCCA	CCCGCCATGG	GGAATGTNCT	CAAGGAATCG	CNGGGCAACG	420
TGGACTCTNG	TCCCNNAAAGG	GGGCAGAATC	TCCAATAGAN	GGANNGAAC	CTTGCTNANA	480
AAAAAAAANA	AAAAAA	AAA	AAA	AAA	AAA	495

## (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 472 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCATT	TTGTCTGCTC	60
CCTCTGGAAG	CCTTGCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATTT	120
TAGCTGTTT	GAGTGATT	GCACCACTGC	ACCACAACTC	AATATGAAAA	CTATTTNACT	180
TATTTATTAT	CTTGTGAAAA	GTATACAATG	AAAATTTGT	TCATACTGTA	TTTATCAAGT	240
ATGATGAAAA	GCAATAGATA	TATATTCTTT	TATTAIGTTN	AATTATGATT	GCCATTATTA	300
ATCGGCAAAA	TGTGGAGTGT	ATGTTCTTT	CACAGTAATA	TATGCCTTT	GTAACCTTCAC	360
TTGGTTATTT	TATTGTAAAT	GAATTACAAA	ATTCTTAATT	TAAGAAAATG	GTANGTTATA	420
TTTANTTCAN	TAATTCTTT	CCTTGTAC	GTTAATTTG	AAAAGAATGC	AT	472

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 476 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTGAAGCATT	TCTTCAAAC	TNTCTACTTT	TGTCATTGAT	ACCTGTAGTA	AGTTGACAAT	60
GTGGTGAAAT	TTCAAAATTA	TATGTAAC	CTACTAGTTT	TAC	TTCTCC	120
TTTTAACTCA	TGATTTTAC	ACACACAATC	CAGAACTTAT	TATATAGCCT	CTAAGTCTT	180
ATTCTTCACA	GTAGATGATG	AAAGAGTCCT	CCAGTGTCTT	GNGCANAATG	TTCTAGNTAT	240
AGCTGGATAC	ATACNGTGGG	AGTTCTATAA	ACTCATACCT	CAGTGGGACT	NAACCAAAT	300
TGTGTTAGTC	TCAATTCTCA	CCACACTGAG	GGAGCCTCCC	AAATCACTAT	ATTCTTATCT	360
GCAGGTACTC	CTCCAGAAAA	ACNGACAGGG	CAGGCTTGCA	TGAAAAAGTN	ACATCTGCGT	420
TACAAAGTCT	ATCTTCCTCA	NANGTCTGTN	AAGGAACAAT	TTAATCTTCT	AGCTTT	476

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 479 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACTCTTCTA ATGCTGATAT GATCTGAGT ATAAGAATGC ATATGTCACT AGAATGGATA	60
AAATAATGCT GCAAACCTAA TGTTCTTATG CAAAATGGAA CGCTAATGAA ACACAGCTTA	120
CAATCGAAA TCAAAACTCA CAAGTGCTCA TCTGTTGTAG ATTTAGTGTAA ATAAGACTTA	180
GATTGTGCTC CTTCGGATAT GATTGTTCT CANATCTGG GCAATNTTCC TTAGTCAAAT	240
CAGGCTACTA GAATTCTGTT ATTGGATATN TGAGAGCATG AAATTTTAA NAATACACTT	300
GTGATTATNA AATTAATCAC AAATTCACT TATACTGCT ATCAGCAGCT AGAAAAACAT	360
NTNNNTTTA NATCAAAGTA TTTGTGTTT GGAANTGTNN AAATGAAATC TGAATGTGGG	420
TTCNATCTTA TTTTTCCCN GACNACTANT TNCTTTTTA GGGNCTATTG TGANCCATC	479

## (2) INFORMATION FOR SEQ ID NO:98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTGT GGCACTGACA ATCAGACCTA	60
TGCTAGTTCC TGTCACTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA	120
TCAACTCCAG CTGGATTATT TTGGAGCCTG CAAATCTATT CCTACTTGTAA CGGACTTTGA	180
AGTGATTTCAG TTTCCTCTAC GGATGAGAGA CTGGCTCAAG AATATCCTCA TGCAGCTTTA	240
TGAAGCCACT CTGAACACGC TGGTTATCTA GATGAGAACAA GAGAAATAAA GTCAGAAAAT	300
TTACCTGGAG AAAAGAGGCT TTGGCTGGGG ACCATCCCCT TGAACCTTCT CTTAAGGACT	360
TTAAGAAAAA CTACCACATG TTGTGTATCC TGGTGCCGGC CGTTTATGAA CTGACCACCC	420
TTTGGAAATAA TCTTGACGCT CCTGAACCTTG CTCCTCTGCG A	461

## (2) INFORMATION FOR SEQ ID NO:99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGGCCGCGC GCAGGTGTTT CCTCGTACCG CAGGGCCCCC TCCCTTCCCC AGGCGTCCCT	60
CGGCGCCTCT CGGGGCCCGA GGAGGAGCGG CTGGCGGGTG GGGGGAGTGT GACCCACCC	120
CGGTGAGAAA AGCCTTCTCT AGCGATCTGA GAGGCCTGCC TTGGGGGTAC C	171

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGCCGCAAG	TGCAACTCCA	GCTGGGGCCG	TGCGGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTGCGAC	GACGGCGGCG	GCGACAGTCG	CAGGTGCAGC	GCAGGGCGCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCCGCA	GAGGTCGTGT	CACGTCCCAC	GACCTTGACG	CCGTCGGGGA	180
CAGCCGGAAC	AGAGCCCGGT	GAAGCGGGAG	GCCTCGGGGA	GCCCCTCGGG	AAGGGCGGCC	240
CGAGAGATAAC	GCAGGGTGCAG	GTGGCCGCC				269

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTTTTTTT	TTTTGGAATC	TACTGCGAGC	ACAGCAGGTC	AGCAACAAAGT	TTATTTGCA	60
GCTAGCAAGG	TAACAGGGTA	GGGCATGGTT	ACATGTTCA	GTCAACTTCC	TTTGTCTGG	120
TTGATTGGTT	TGTCTTTATG	GGGGCGGGGT	GGGGTAGGGG	AAACGAAGCA	AATAACATGG	180
AGTGGGTGCA	CCCTCCCTGT	AGAACCTGGT	TACAAAGCTT	GGGGCAGTTC	ACCTGGTCTG	240
TGACCGTCAT	TTCTTGACA	TCAATGTTAT	TAGAAGTCAG	GATATCTTTT	AGAGAGTCCA	300
CTGTTCTGGA	GGGAGATTAG	GGTTTCTTGC	CAAATCCAAC	AAAATCCACT	GAAAAAGTTG	360
GATGATCAGT	ACGAATACCG	AGGCATATTC	TCATATCGGT	GGCCA		405

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
GGCACTTAAT	CCATTTTAT	TTCAAAATGT	CTACAAATT	AATCCCATT	TACGGTATT	120
TCAAAATCTA	AATTATTCAA	ATTAGCCAAA	TCCTTACCAA	ATAATACCCA	AAAATCAAAA	180
ATATACTTCT	TTCAGCAAAC	TTGTTACATA	AATTAAAAAA	ATATATACGG	CTGGTGTGTT	240
CAAAGTACAA	TTATCTTAAC	ACTGCAAACA	TTTTAAGGAA	CTAAAATAAA	AAAAAACACT	300

CCGCAAAGGT TAAAGGGAAC AACAAATTCT TTTACAACAC CATTATAAAA ATCATATCTC	360
AAATCTTAGG GGAATATATA CTTCACACGG GATCTTAACT TTTACTCACT TTGTTTATTT	420
TTTAAACCA TTGTTGGGC CCAACACAAT GGAATCCCCC CTGGACTAGT	470

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TTTTTTTTTT TTTTTTTG A CCCCCCTCTT ATAAAAAACA AGTTACCATT TTATTTACT	60
TACACATATT TATTTTATAA TTGGTATTAG ATATTCAAAA GGCAGCTTT AAAATCAAAC	120
TAAATGGAAA CTGCCTTAGA TACATAATTC TTAGGAATTA GCTTAAAATC TGCTAAAGT	180
GAAAATCTTC TCTAGCTCTT TTGACTGTAA ATTTTGACT CTTGTAAAAC ATCCAAATTC	240
ATTTTTCTTG TCTTTAAAAT TATCTAATCT TTCCATTTT TCCCTATTCC AAGTCAATT	300
GCTTCTCTAG CCTCATTTC TAGCTCTTAT CTACTATTAG TAAGTGGCTT TTTTCCTAAA	360
AGGGAAAACA GGAAGAGAAA TGGCACACAA AACAAACATT TTATATTCA ATTCTACCT	420
ACGTTAATAA AATAGCATT TGTGAAGCCA GCTAAAAGA AGGCTTAGAT CCTTTATGT	480
CCATTTAGT CACTAACCGA TATCAAAGTG CCAGAACGCA AAAGGTTGT GAACATTAT	540
TCAAAAGCTA ATATAAGATA TTTCACATAC TCATCTTCT G	581

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTTTTTTTTT TTTTTCTCTT CTTTTTTTTT GAAATGAGGA TCGAGTTTT	60
CACTCTCTAG ATAGGGCATG AAGAAAATC ATCTTCCAG CTTTAAAATA ACAATCAAAT	120
CTCTTATGCT ATATCATATT TTAAGTTAAA CTAATGAGTC ACTGGCTTAT CTTCTCCTGA	180
AGGAAATCTG TTCATTCTTC TCATTCATAT AGTTATATCA AGTACTACCT TGCATATTGA	240
GAGGTTTTTC TTCTCTATT ACACATATAT TTCCATGTGA ATTTGTATCA AACCTTTATT	300
TTCATGAAA CTAGAAAATA ATGTTCTTT TGCATAAGAG AAGAGAACAA TATAGCATTA	360
CAAAACTGCT CAAATTGTTT GTTAAGTTAT CCATTATAAT TAGTTGGCAG GAGCTAATAC	420
AAATCACATT TACGACAGCA ATAATAAAAC TGAAGTACCA GTTAAATATC CAAAATAATT	480
AAAGGAACAT TTTAGCCTG GGTATAATTA GCTAATTAC TTTACAAGCA TTTATTAGAA	540
TGAATTACCA TGTTATTATT CCTAGCCCAA CACAATGG	578

(2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TTTTTTTTT	TTTTTCAGTA	ATAATCAGAA	CAATATTTAT	TTTTATATT	AAAATTCATA	60
GAAAAGTGCC	TTACATTTAA	TAAAAGTTG	TTTCTCAAAG	TGATCAGAGG	AATTAGATAT	120
GTCTTGAACA	CCAATATTAA	TTTGAGGAAA	ATACACCAAA	ATACATTAAG	TAAATTATTT	180
AAGATCATAG	AGCTTGTAAG	TGAAAAGATA	AAATTGACC	TCAGAAACTC	TGAGCATTAA	240
AAATCCACTA	TTAGCAAATA	AATTACTATG	GACTTCTTGC	TTTAATTG	TGATGAATAT	300
GGGGTGTAC	TGGTAAACCA	ACACATTCTG	AAGGATACAT	TACTTAGTGA	TAGATTCTTA	360
TGTACTTTGC	TAATACGTGG	ATATGAGTTG	ACAAGTTCT	CTTCTTCAA	TCTTTAAGG	420
GGCGAGAAAT	GAGGAAGAAA	AGAAAAGGAT	TACGCATACT	GTTCTTCTA	TGGAAGGATT	480
AGATATGTTT	CCTTGCCAA	TATTAACAAA	ATAATAATGT	TTACTACTAG	TGAAACCC	538

(2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TTTTTTTTT	TTTTTAGTC	AAGTTCTAT	TTTTATTATA	ATTAAAGTCT	TGGTCATTTC	60
ATTTATTAGC	TCTGCAACTT	ACATATTTAA	ATTAAAGAAA	CGTTTAGAC	AACTGTACAA	120
TTTATAAATG	TAAGGTGCCA	TTATTGAGTA	ATATATTCT	CCAAGAGTGG	ATGTGTCCCT	180
TCTCCCACCA	ACTAATGAAC	AGCAACATTA	GTAAATT	ATTAGTAGAT	ATACACTGCT	240
GCAAACGCTA	ATTCTCTTCT	CCATCCCCAT	GTGATATTGT	GTATATGTGT	GAGTTGGTAG	300
AATGCATCAC	AATCTACAAT	CAACAGCAAG	ATGAAGCTAG	GCTGGGCTTT	CGGTGAAAAT	360
AGACTGTGTC	TGTCTGAATC	AAATGATCTG	ACCTATCCTC	GGTGGCAAGA	ACTCTTCGAA	420
CCGCTTCCTC	AAAGGCGCTG	CCACATTTGT	GGCTCTTGC	ACTTGTTCA	AAA	473

(2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107;

CGCCATGGCA	CTGCAGGGCA	TCTCGGTCA	GGAGCTGTCC	GGCCTGGCCC	CGGGCCCGTT	60
CTGTGCTATG	GTCCTGGCTG	ACTTCGGGGC	GCGTGTGGTA	CGCGTGGACC	GGCCCGGCTC	120
CCGCTACGAC	GTGAGCCGCT	TGGGCCGGGG	CAAGCGCTCG	CTAGTGCTGG	ACCTGAAGCA	180
GCCGCGGGGA	GCCGCCGTGC	TGCGCGTCT	GTGCAAGCGG	TCGGATGTGC	TGCTGGAGCC	240
CTTCCGCCGC	GGTGTCACTGG	AGAAACTCCA	GCTGGGCCCA	GAGATTCTGC	AGCAGGAAAAA	300
TCCAAGGCTT	ATTATATGCCA	GGCTGAGTGG	ATTGGCCAG	TCAGGAAGCT	TCTGCCGGTT	360
AGCTGGCCAC	GATATCAACT	ATTGGCTTT	GTCAGGTGTT	CTCTCAAAAAA	TTGGCAGAAG	420
TGGTGAGAAT	CCGTATGCC	CGCTGAATCT	CCTGGCTGAC	TTTGCTGGTG	GTGGCCTTAT	480
GTGTGCACTG	GGCATTATAA	TGGCTCTTTT	TGACCGCACA	CGCACTGACA	AGGGTCAGGT	540
CATTGATGCA	AATATGGTGG	AAGGAACAGC	ATATTAAAGT	TCTTTCTGT	GGAAAACCTCA	600
GAAATCGAGT	CTGTGGGAAG	CACCTCGAGG	ACAGAACATG	TTGGATGGTG	GAGCACCTTT	660
CTATACGACT	TACAGGACAG	CAGATGGGG	ATTCATGGCT	GTTGGAGCAA	TAGAACCCCA	720
GTTCTACGAG	CTGCTGATCA	AAGGACTTGG	ACTAAAGTCT	GATGAACCTC	CCAATCAGAT	780
GAGCATGGAT	GATTGGCCAG	AAATGAAGAA	GAAGTTTGCA	GATGTATTG	CAAAGAAGAC	840
GAAGGCAGAG	TGGTGTCAAA	TCTTGACGG	CACAGATGCC	TGTGTGACTC	CGGTTCTGAC	900
TTTGAGGAG	GTTGTTCATC	ATGATCACAA	CAAGGAACGG	GGCTCGTTA	TCACCCAGTGA	960
GGAGCAGGAC	GTGAGCCCCC	GCCCTGCACC	TCTGCTGTTA	AACACCCAG	CCATCCCTTC	1020
TTTCAAAAGG	GATCCTTCA	TAGGAGAACAA	CACTGAGGAG	ATACTTGAAG	AATTGGATT	1080
CAGCCCGGAA	GAGATTATC	AGCTTAAC	AGATAAAATC	ATTGAAAGTA	ATAAGGTAAA	1140
AGCTAGTCTC	TAACCTCCAG	GCCCACGGCT	CAAGTGAATT	TGAATACTGC	ATTTACAGTG	1200
TAGAGTAACA	CATAACATTG	TATGCATGGA	AACATGGAGG	AACAGTATTA	CAGTGTCC	1260
CCACTCTAAT	CAAGAAAAGA	ATTACAGACT	CTGATTCTAC	AGTGATGATT	GAATTCTAAA	1320
AATGGTTATC	ATTAGGGCTT	TTGATTATA	AAACTTTGGG	TACTTATACT	AAATTATGGT	1380
AGTTATTCTG	CCTTCCAGTT	TGCTTGATAT	ATTGTTGAT	ATTAAGATTC	TTGACTTATA	1440
TTTGAAATGG	GTTCTAGTGA	AAAAGGAATG	ATATATTCTT	GAAGACATCG	ATATACATT	1500
ATTTACACTC	TTGATTCTAC	AATGTAGAAA	ATGAGGAAAT	GCCACAAATT	GTATGGTGT	1560
AAAAGTCACG	TGAAACAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1620
A						1621

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met	Ala	Leu	Gln	Gly	Ile	Ser	Val	Met	Glu	Leu	Ser	Gly	Leu	Ala	Pro
1				5					10					15	
Gly	Pro	Phe	Cys	Ala	Met	Val	Leu	Ala	Asp	Phe	Gly	Ala	Arg	Val	Val
					20				25				30		
Arg	Val	Asp	Arg	Pro	Gly	Ser	Arg	Tyr	Asp	Val	Ser	Arg	Leu	Gly	Arg
						35		40			45				
Gly	Lys	Arg	Ser	Leu	Val	Leu	Asp	Leu	Lys	Gln	Pro	Arg	Gly	Ala	Ala
						50		55			60				
Val	Leu	Arg	Arg	Leu	Cys	Lys	Arg	Ser	Asp	Val	Leu	Leu	Glu	Pro	Phe
						65		70			75				80

Arg	Arg	Gly	Val	Met	Glu	Lys	Leu	Gln	Leu	Gly	Pro	Glu	Ile	Leu	Gln
				85					90						95
Arg	Glu	Asn	Pro	Arg	Leu	Ile	Tyr	Ala	Arg	Leu	Ser	Gly	Phe	Gly	Gln
				100				105						110	
Ser	Gly	Ser	Phe	Cys	Arg	Leu	Ala	Gly	His	Asp	Ile	Asn	Tyr	Leu	Ala
				115			120					125			
Leu	Ser	Gly	Val	Leu	Ser	Lys	Ile	Gly	Arg	Ser	Gly	Glu	Asn	Pro	Tyr
				130		135			140						
Ala	Pro	Leu	Asn	Leu	Leu	Ala	Asp	Phe	Ala	Gly	Gly	Gly	Leu	Met	Cys
				145		150			155					160	
Ala	Leu	Gly	Ile	Ile	Met	Ala	Leu	Phe	Asp	Arg	Thr	Arg	Thr	Asp	Lys
					165			170					175		
Gly	Gln	Val	Ile	Asp	Ala	Asn	Met	Val	Glu	Gly	Thr	Ala	Tyr	Leu	Ser
				180			185					190			
Ser	Phe	Leu	Trp	Lys	Thr	Gln	Lys	Ser	Ser	Leu	Trp	Glu	Ala	Pro	Arg
				195			200				205				
Gly	Gln	Asn	Met	Leu	Asp	Gly	Gly	Ala	Pro	Phe	Tyr	Thr	Thr	Tyr	Arg
				210			215			220					
Thr	Ala	Asp	Gly	Glu	Phe	Met	Ala	Val	Gly	Ala	Ile	Glu	Pro	Gln	Phe
				225		230			235					240	
Tyr	Glu	Leu	Leu	Ile	Lys	Gly	Leu	Gly	Leu	Lys	Ser	Asp	Glu	Leu	Pro
					245			250					255		
Asn	Gln	Met	Ser	Met	Asp	Asp	Trp	Pro	Glu	Met	Lys	Lys	Lys	Phe	Ala
				260			265				270				
Asp	Val	Phe	Ala	Lys	Lys	Thr	Lys	Ala	Glu	Trp	Cys	Gln	Ile	Phe	Asp
				275			280				285				
Gly	Thr	Asp	Ala	Cys	Val	Thr	Pro	Val	Leu	Thr	Phe	Glu	Glu	Val	Val
				290			295			300					
His	His	Asp	His	Asn	Lys	Glu	Arg	Gly	Ser	Phe	Ile	Thr	Ser	Glu	Glu
				305			310			315				320	
Gln	Asp	Val	Ser	Pro	Arg	Pro	Ala	Pro	Leu	Leu	Leu	Asn	Thr	Pro	Ala
				325				330					335		
Ile	Pro	Ser	Phe	Lys	Arg	Asp	Pro	Phe	Ile	Gly	Glu	His	Thr	Glu	Glu
				340				345				350			
Ile	Leu	Glu	Glu	Phe	Gly	Phe	Ser	Arg	Glu	Glu	Ile	Tyr	Gln	Leu	Asn
				355			360				365				
Ser	Asp	Lys	Ile	Ile	Glu	Ser	Asn	Lys	Val	Lys	Ala	Ser	Leu		
				370			375			380					

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

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GGCACGAGGC TGCAGCCAGGG CCTGAGCGGA GGCGGGGGCA GCCTCGCCAG CGGGGGCCCC 60
GGGCCTGGCC ATGCCTCACT GAGCCAGCGC CTGCGCCTCT ACCTCGCCGA CAGCTGGAAC 120
CAGTGCGACC TAGTGGCTCT CACCTGCTTC CTCTGGGCG TGCGCTGCCG GCTGACCCCG 180
GGTTTGTACC ACCTGGGCCG CACTGTCCCTC TGCATCGACT TCATGGTTTT CACGGTGCGG 240

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CTGCTTCACA	TCTTCACGGT	CAACAAACAG	CTGGGGCCCA	AGATCGTCAT	CGTGAGCAAG	300
ATGATGAAGG	ACGTGTTCTT	CTTCCTCTTC	TTCCTCGGCG	TGTGGCTGGT	AGCCTATGGC	360
GTGGCCACGG	AGGGGCTCCT	GAGGCCACGG	GACAGTGA	TCCCAAGTAT	CCTGCGCCGC	420
GTCTTCTACC	GTCCCTACCT	GCAGATCTTC	GGGCAGATT	CCCAGGAGGA	CATGGACGTG	480
GCCCTCATGG	AGCACAGCAA	CTGCTCGTCG	GAGCCCGGCT	TCTGGGCACA	CCCTCCTGGG	540
GCCCAGGCGG	GCACCTGCGT	CTCCCAGTAT	GCCAACTGGC	TGGTGGTGT	GCTCCTCGTC	600
ATCTTCCTGC	TCGTGGCCAA	CATCCTGCTG	GTCAA	TCATTGCCAT	GTTAGTTAC	660
ACATTGGCA	AAGTACAGGG	CAACAGCGAT	CTCTACTGGA	AGGCGCAGCG	TTACCGCCTC	720
ATCCGGGAAT	TCCACTCTCG	GCCCCGCGT	GCCCCGCCCT	TTATCGTCAT	CTCCCAC	780
CGCCTCCTGC	TCAGGCAATT	GTGCAGGCGA	CCCCGGAGCC	CCCAGCCGTC	CTCCCCGGCC	840
CTCGAGCATT	TCCGGGTTA	CCTTCTAAG	GAAGCCGAGC	GGAAGCTGCT	AACGTGGAA	900
TCGGTGCATA	AGGAGAACTT	TCTGCTGGCA	CGCGCTAGGG	ACAAGCGGGA	GAGCGACTCC	960
GAGCGTCTGA	AGCGCACGTC	CCAGAAGGTG	GA	TGAAACAGCT	GGGACACATC	1020
CGCGAGTACG	AACAGCGCCT	GAAAGTGCTG	GAGCGGGAGG	TCCAGCAGTG	TAGCCGCGTC	1080
CTGGGGTGGG	TGGCCGAGGC	CCTGAGCCGC	TCTGCTTGC	TGCC	TGGGCCGCCA	1140
CCCCCTGACC	TGCCTGGGTC	CAAAGACTGA	GCCCTGCTGG	CGGACTTCAA	GGAGAAGCCC	1200
CCACAGGGGA	TTTGCTCCT	AGAGTAAGGC	TCATCTGGGC	CTCGGCCCCC	GCACCTGGTG	1260
GCCTTGTCT	TGAGGTGAGC	CCCATGTCCA	TCTGGGCCAC	TGTCAGGACC	ACCTTTGGGA	1320
GTGTCAATCCT	TACAAACCAC	AGCATGCCCG	GCTCCTCCCA	GAACCAGTCC	CAGCCTGGGA	1380
GGATCAAGGC	CTGGATCCCC	GGCCGTTATC	CATCTGGAGG	CTGCAGGGTC	CTTGGGGTAA	1440
CAGGGACCAC	AGACCCCTCA	CCACTCACAG	ATTCTCACA	CTGGGAAAT	AAAGCCATT	1500
CAGAGGAAAA	AAAAAAA	AAAA				1524

## (2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGGAACCAGC	CTGCACGCGC	TGGCTCCGGG	TGACAGCCGC	GCGCCTCGGC	CAGGATCTGA	60
GTGATGAGAC	GTGTCCCCAC	TGAGGTGCC	CACAGCAGCA	GGTGTGAGC	ATGGGCTGAG	120
AAGCTGGACC	GGCACCAAAG	GGCTGGCAGA	AATGGGCGCC	TGGCTGATT	CTAGGCAGTT	180
GGCGCAGCA	AGGAGGAGAG	GCCGCAGCTT	CTGGAGCAGA	GCCGAGACGA	AGCAGTTCTG	240
GAGTGCCTGA	ACGGCCCCCT	GAGCCCTACC	CGCCTGGCC	ACTATGGTCC	AGAGGCTGTG	300
GGTGAGCCGC	CTGCTCGGGC	ACCGGAAAGC	CCAGCTCTTG	CTGGTCAACC	TGCTAACCTT	360
TGGCCTGGAG	GTGTGTTGG	CCGCAGGCAT	CACCTATGTG	CCGCCTCTGC	TGCTGGAAGT	420
GGGGGTAGAG	GAGAAGTTCA	TGACCATGGT	GCTGGGCATT	GGTCCAGTGC	TGGGCCTGGT	480
CTGTGTCCCG	CTCCTAGGCT	CAGCCAGTGA	CCACTGGCGT	GGACGCTATG	GCCGCCGCCG	540
GCCCTTCATC	TGGGCACTGT	CCTGGGCAT	CCTGCTGAGC	CTCTTCTCA	TCCCAAGGGC	600
CGGCTGGCTA	GCAGGGCTGC	TGTGCCCGGA	TCCCAGGCC	CTGGAGCTGG	CACTGCTCAT	660
CCTGGCGTG	GGGCTGCTGG	ACTTCTGTGG	CCAGGTGTGC	TTCACTCCAC	TGGAGGCCCT	720
GCTCTCTGAC	CTCTTCCGGG	ACCCGGACCA	CTGTCGCCAG	GCCTACTCTG	TCTATGCCTT	780
CATGATCAGT	CTTGGGGGCT	GCCTGGGCTA	CCTCCTGCCT	GCCATTGACT	GGGACACCAG	840
TGCCCTGGCC	CCCTACCTGG	GCACCCAGGA	GGAGTGCCTC	TTTGGCCTGC	TCACCCTCAT	900
CTTCCTCACC	TGCGTAGCAG	CCACACTGCT	GGTGGCTGAG	GAGGCAGCGC	TGGGCCAAC	960
CGAGCCAGCA	GAAGGGCTGT	CGGCCCCCTC	CTTGTGCGCC	CACTGCTGTC	CATGCCGGGC	1020
CCGCTTGGCT	TTCCGGAACC	TGGCGCCCT	GCTTCCCCGG	CTGCACCAGC	TGTGCTGCCG	1080
CATGCCCGC	ACCCTGCGCC	GGCTCTTCGT	GGCTGAGCTG	TGCAGCTGGA	TGGCACTCAT	1140
GACCTTCACG	CTGTTTACA	CGGATTCGT	GGCGAGGGGG	CTGTACCAAGG	CGGTGCCAG	1200

AGCTGAGCCG	GGCACCGAGG	CCCGGAGACA	CTATGATGAA	GGCGTCGGA	TGGGCAGCCT	1260
GGGGCTGTC	CTGCAGTGC	CCATCTCCCT	GGTCTTCTCT	CTGGTCATGG	ACCGGCTGGT	1320
GCAGCGATT	GGCACTCGAG	CAGTCTATT	GGCCAGTGTG	GCAGCTTCC	CTGTGGCTGC	1380
CGGTGCCACA	TGCCTGTCCC	ACAGTGTGGC	CGTGGTGACA	GCTTCAGCCG	CCCTCACCGG	1440
GTTCACCTC	TCAGCCCTGC	AGATCCTGCC	CTACACACTG	GCCTCCCTCT	ACCACCGGGA	1500
GAAGCAGGTG	TTCCTGCCA	AATACCGAGG	GGACACTGGA	GGTGCTAGCA	GTGAGGACAG	1560
CCTGATGACC	AGCTTCCTGC	CAGGCCCTAA	GCCTGGAGCT	CCCTTCCCTA	ATGGACACGT	1620
GGGTGCTGGA	GGCAGTGGCC	TGCTCCCACC	TCCACCCGCG	CTCTGCGGGG	CCTCTGCCTG	1680
TGATGTCTCC	GTACGTGTGG	TGGTGGGTGA	GCCCACCGAG	GCCAGGGTGG	TTCCGGGCCG	1740
GGGCATCTGC	CTGGACCTCG	CCATCCTGGA	TAGTGCCTTC	CTGCTGTCCC	AGGTGGCCCC	1800
ATCCCTGTT	ATGGGCTCCA	TTGTCCAGCT	CAGCCAGTCT	GTCACTGCCT	ATATGGTGTG	1860
TGCCGCAGGC	CTGGGTCTGG	TCGCCATT	CTTGCTACA	CAGGTAGTAT	TTGACAAGAG	1920
CGACTTGGCC	AAATACTCAG	CGTAGAAAAC	TTCCAGCACA	TTGGGGTGG	GGGCCTGCCT	1980
CACTGGGTCC	CAGCTCCCCG	CTCCTGTTAG	CCCCATGGGG	CTGCCGGGCT	GGCGGCCAGT	2040
TTCTGTTGCT	GCCAAAGTAA	TGTGGCTCTC	TGCTGCCACC	CTGTGCTGCT	GAGGTGCGTA	2100
GCTGCACAGC	TGGGGGCTGG	GGCGTCCCTC	TCCTCTCTCC	CCAGTCTCTA	GGGCTGCCTG	2160
ACTGGAGGCC	TTCCAAGGGG	TTTCAGTCT	GGACTTATAC	AGGGAGGCCA	GAAGGGCTCC	2220
ATGCACTGGA	ATGCAGGGAC	TCTGCAGGTG	GATTACCCAG	GCTCAGGGTT	AACAGCTAGC	2280
CTCCTAGTTG	AGACACACCT	AGAGAAGGGT	TTTGGGAGC	TGAATAAACT	CAGTCACCTG	2340
GTTTCCCATC	TCTAACCCCC	TTAACCTGCA	GCTTCGTTA	ATGTAGCTCT	TGCATGGGAG	2400
TTTCTAGGAT	GAAACACTCC	TCCATGGGAT	TTGAACATAT	GAATTATTG	TAGGGGAAGA	2460
GTCCTGAGGG	GCAACACACA	AGAACCAAGGT	CCCCTCAGCC	CACAGCACTG	TCTTTTGCT	2520
GATCCACCCC	CCTCTTACCT	TTTATCAGGA	TGTGGCTGT	TGGCCTTCT	GTTGCCATCA	2580
CAGAGACACA	GGCATTAAA	TATTAACTT	ATTATTAA	CAAAGTAGAA	GGGAATCCAT	2640
TGCTAGCTT	TCTGTGTTGG	TGTCTAATAT	TTGGGTAGGG	TGGGGGATCC	CCAACAATCA	2700
GGTCCCCCTGA	GATAGCTGGT	CATTGGGCTG	ATCATTGCCA	GAATCTTCTT	CTCCTGGGGT	2760
CTGGCCCCCC	AAAATGCCTA	ACCCAGGACC	TTGGAAATT	TACTCATCCC	AAATGATAAT	2820
TCCAAATGCT	GTTACCAAG	GTTAGGGTGT	TGAAGGAAGG	TAGAGGGTGG	GGCTTCAGGT	2880
CTCAACGGCT	TCCCTAACCA	CCCCTCTTCT	CTTGGCCAG	CCTGGTTCCC	CCCACTTCCA	2940
CTCCCCCTCA	CTCTCTCTAG	GAATGGGCTG	ATGAAGGCAC	TGCCCAAAAT	TTCCCTTACC	3000
CCCAACTTTC	CCCTACCCCC	AACTTCCCC	ACCAGCTCCA	CAACCCTGTT	TGGAGCTACT	3060
GCAGGACCAG	AAGCACAAAG	TGCGGTTCC	CAAGCCTTG	TCCATCTCAG	CCCCCAGAGT	3120
ATATCTGTG	TTGGGGAATC	TCACACAGAA	ACTCAGGAGC	ACCCCTGCC	TGAGCTAAGG	3180
GAGGTCTTAT	CTCTCAGGGG	GGGTTTAAGT	GCCGTTTGCA	ATAATGTCGT	CTTATTATT	3240
TAGCGGGGTG	AATATTAT	ACTGTAAGTG	AGCAATCAGA	GTATAATGTT	TATGGTGACA	3300
AAATTAAAGG	CTTTCTTATA	TGTTAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	3360
AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAATAA	AAAAAAAAAA	AAAAAAAAAA	3410

## (2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1289 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCCAGGC	CCCTCTGCCT	GCCCACTCAG	TGGCAACACC	CGGGAGCTGT	TTTGTCTTT	60
GTGGAGC	CTCAGTTCCC	TCTTCAGAA	CTCACTGCCA	AGAGCCCTGA	ACAGGAGCCA	120
CCATGCAG	CTTCAGCTTC	ATTAAGACCA	TGATGATCCT	CTTCAATTG	CTCATCTTTC	180
TGTGTGG	AGCCCTGTTG	GCAGTGGGCA	TCTGGGTGTC	AATCGATGGG	GCATCCTTTC	240
TGAAGATCT	CGGGCCACTG	TCGTCCAGTG	CCATGCAGTT	TGTCAACGTG	GGCTACTTCC	300

TCATCGCAGC	CGGCGTTGTG	GTCTTGCTC	TTGGTTCCCT	GGGCTGCTAT	GGTGCTAAGA	360
CTGAGAGCAA	GTGTGCCCTC	GTGACGTTCT	TCTTCATCCT	CCTCCTCATC	TTCATTGCTG	420
AGGTTGCAGC	TGCTGTGGTC	GCCTTGGTGT	ACACCACAAT	GGCTGAGCAC	TTCCTGACGT	480
TGCTGGTAGT	GCCTGCCATC	AAGAAAGATT	ATGGTTCCCA	GGAAGACTTC	ACTCAAGTGT	540
GGAACACACCAC	CATGAAAGGG	CTCAAGTGCT	GTGGCTTCAC	CAACTATAACG	GATTTTGAGG	600
ACTCACCCCTA	CTTCAAAGAG	AACAGTGCTT	TTCCCCCATT	CTGTTGCAAT	GACAACGTCA	660
CCAACACAGC	CAATGAAACC	TGCACCAAGC	AAAAGGCTCA	CGACCAAAAA	GTAGAGGGTT	720
GCTTCAATCA	GCTTTGTAT	GACATCCGAA	CTAATGCAGT	CACCGTGGGT	GGTGTGGCAG	780
CTGGAATTGG	GGGCCTCGAG	CTGGCTGCCA	TGATTGTGTC	CATGTATCTG	TACTGCAATC	840
TACAATAAGT	CCACTTCTGC	CTCTGCCACT	ACTGCTGCCA	CATGGGAACT	GTGAAGAGGC	900
ACCCTGGCAA	GCAGCAGTGA	TTGGGGGAGG	GGACAGGATC	TAACAATGTC	ACTTGGGCCA	960
GAATGGACCT	GCCCTTCTG	CTCCAGACTT	GGGGCTAGAT	AGGGACCACT	CCTTTTAGCG	1020
ATGCCTGACT	TTCCTTCCAT	TGGTGGGTGG	ATGGGTGGGG	GGCATTCCAG	AGCCTCTAAG	1080
GTAGCCAGTT	CTGTTGCCA	TTCCCCCAGT	CTATTAAACC	CTTGATATGC	CCCCTAGGCC	1140
TAGTGGTGAT	CCCAGTGCTC	TACTGGGGGA	TGAGAGAAAG	GCATTTATA	GCCTGGGCAT	1200
AAGTGAAATC	AGCAGAGCCT	CTGGGTGGAT	GTGTAGAAGG	CACTTCAAAA	TGCATAAAACC	1260
TGTTACAATG	TTAAAAAAAAA	AAAAAAA				1289

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met	Val	Phe	Thr	Val	Arg	Leu	Leu	His	Ile	Phe	Thr	Val	Asn	Lys	Gln
1									10						15

Leu	Gly	Pro	Lys	Ile	Val	Ile	Val	Ser	Lys	Met	Met	Lys	Asp	Val	Phe
									25						30

Phe	Phe	Leu	Phe	Phe	Leu	Gly	Val	Trp	Leu	Val	Ala	Tyr	Gly	Val	Ala
									40						45

Thr	Glu	Gly	Leu	Leu	Arg	Pro	Arg	Asp	Ser	Asp	Phe	Pro	Ser	Ile	Leu
									55						60

Arg	Arg	Val	Phe	Tyr	Arg	Pro	Tyr	Leu	Gln	Ile	Phe	Gly	Gln	Ile	Pro
									65						80

Gln	Glu	Asp	Met	Asp	Val	Ala	Leu	Met	Glu	His	Ser	Asn	Cys	Ser	Ser
									85						95

Glu	Pro	Gly	Phe	Trp	Ala	His	Pro	Pro	Gly	Ala	Gln	Ala	Gly	Thr	Cys
									100						110

Val	Ser	Gln	Tyr	Ala	Asn	Trp	Leu	Val	Val	Leu	Leu	Leu	Val	Ile	Phe
									115						125

Leu	Leu	Val	Ala	Asn	Ile	Leu	Leu	Val	Asn	Leu	Leu	Ile	Ala	Met	Phe
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

130	135	140
Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys		
145	150	155
Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu		
165	170	175
Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln		
180	185	190
Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu		
195	200	205
His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr		
210	215	220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp		
225	230	235
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val		
245	250	255
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg		
260	265	270
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly		
275	280	285
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly		
290	295	300
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp		
305	310	315

## (2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met	Val	Gln	Arg	Leu	Trp	Val	Ser	Arg	Leu	Leu	Arg	His	Arg	Lys	Ala
1				5				10				15			
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu															
				20				25				30			
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val															
				35				40				45			

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
 50 55 60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly  
 65 70 75 80

Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile  
 85 90 95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
 100 105 110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly  
 115 120 125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
 130 135 140

Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
 145 150 155 160

Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
 165 170 175

Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
 180 185 190

Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
 195 200 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly  
 210 215 220

Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His  
 225 230 235 240

Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu  
 245 250 255

Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg  
 260 265 270

Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
 275 280 285

Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
 290 295 300

Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
 305 310 315 320

Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
 325 330 335

Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
 340 345 350

Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
 355 360 365  
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
 370 375 380  
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
 385 390 395 400  
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
 405 410 415  
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
 420 425 430  
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
 435 440 445  
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser  
 450 455 460  
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
 465 470 475 480  
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
 485 490 495  
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
 500 505 510  
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
 515 520 525  
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp  
 530 535 540  
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
 545 550

## (2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 241 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
 1 5 10 15  
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val

20	25	30
Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser		
35	40	45
Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly		
50	55	60
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr		
65	70	75
		80
Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile		
85	90	95
Phe Ile Ala Glu Val Ala Ala Val Val Ala Leu Val Tyr Thr Thr		
100	105	110
Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys		
115	120	125
Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met		
130	135	140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp		
145	150	155
		160
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn		
165	170	175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala		
180	185	190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile		
195	200	205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly		
210	215	220
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu		
225	230	235
		240
Gln		

## (2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 366 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTCTTCCTC	TCCCCTCCTC	TGAATTAAAT	TCTTCAACT	TGCAATTGC	AAGGATTACA	60
CATTTCACTG	TGATGTATAT	TGTGTTGCAA	AAAAAAAAAA	GTGTCTTGT	TTAAAATTAC	120
TTGGTTTGTG	AATCCATCTT	GCTTTTCCC	CATTGGAAC	AGTCATTAAC	CCATCTCTGA	180
ACTGGTAGAA	AAACATCTGA	AGAGCTAGTC	TATCAGCATC	TGACAGGTGA	ATTGGATGGT	240
TCTCAGAAC	ATTCACCCA	GACAGCCTGT	TTCTATCCTG	TTTAATAAAT	TAGTTGGGT	300
TCTCTACATG	CATAACAAAC	CCTGCTCCAA	TCTGTCACAT	AAAAGTCTGT	GACTTGAAGT	360
	TTAGTC					366

## (2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 282 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ACAAAGATGA	ACCATTCCT	ATATTATAGC	AAAATTAAAA	TCTACCCGTA	TTCTAATATT	60
GAGAAATGAG	ATNAAACACA	ATNTTATAAA	GTCTACTTAG	AGAAGATCAA	GTGACCTCAA	120
AGACTTTACT	ATTTCATAT	TTTAAGACAC	ATGATTATC	CTATTAGT	AACCTGGTTC	180
ATACGTTAAA	CAAAGGATAA	TGTGAACAGC	AGAGAGGATT	TGTTGGCAGA	AAATCTATGT	240
TCAATCTNGA	ACTATCTANA	TCACAGACAT	TTCTATTCC	TT		282

## (2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ACACATGTCG	CTTCACTGCC	TTCTTAGATG	CTTCTGGTCA	ACATANAGGA	ACAGGGACCA	60
TATTTATCCT	CCCTCCTGAA	ACAATTGCAA	AATAANACAA	AATATATGAA	ACAATTGCAA	120
AATAAGGCAA	AATATATGAA	ACAACAGGTC	TCGAGATATT	GGAAATCAGT	CAATGAAGGA	180
TACTGATCCC	TGATCACTGT	CCTAATGCAG	GATGTGGAA	ACAGATGAGG	TCACCTCTGT	240
GACTGCCCA	GCTTACTGCC	TGTAGAGAGT	TTCTANGCTG	CAGTCAGAC	AGGGAGAAAT	300
	TGGGT					305

## (2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 71 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACCAAGGTGT NTGAATCTCT GACGTGGGGA TCTCTGATTC CCGCACAATC TGAGTGGAAA  
AANTCCTGGG T

60

71

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCACA  
GAAAATGGGG TGAAATTGGC CAACTTCTA TNAACTTATG TTGGCAANTT TGCCACCAAC  
AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCACTAANC GGAATTAANT  
AATGGANTCA AGANACTCCC AGGCCTCAGC GT

60

120

180

212

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ACTCGTTGCA NATCAGGGGC CCCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC  
CTCCGCCGGC GCAGAACATG CTGGGGTGGT

60

90

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGTANC GTGA ANACGACAGA NAGGGTTGTC AAAAATGGAG AACCTTGAA GTCATTTGA	60
GAATAAGATT TGCTAAAAGA TTTGGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG	120
ATATNCANGT AAATTANGGA ATGAATTCAT GGTTCTTTG GGAATTCCCTT TACGATNGCC	180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA	218

- (2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 171 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG	60
CATTTGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT	120
CACCACCCCG GCGGGGTCAT CTGTGCCACA GGTCCCTGTT GACAGTGC GG T	171

- (2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 76 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA	60
TTATCAANTA TTGTGT	76

- (2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 131 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ACCTTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT	60
CAATGTGCTG GGTCAATATGG AGGGGAGGAG ACTCTAAAAT AGCCAATT TTCTCTTGG	120
TTAAGATTTG T	131

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCACTGG	60
CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA	120
CTACAGTCTG CATTGGCAG AAATGAAGAT GAATTTGGAT TAAATGAGGA TGCTGAAGAT	180
TTGCCTCACC AAACAAAAGT GAAACAACTG AGAGAAAATT TTCAGGAAAA AAGACAGTGG	240
CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC	300
CATGGTGGGG GTCTTGCATC TGTAAGAATG GAATTGATTT TGCTTTGCA AGAATCTCAG	360
CAGGAAACAT CAGAACCACT ATTTCTAGC CCTCTGTCAG AGCAAACCTC AGTGCCTCTC	420
CTCTTGCTT GT	432

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACTTG AATAGTAAAA TAGAAACTGA GCTGAAATT CTAATTCACT TTCTAACCAT	60
AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATT ATAAAAATT GT	112

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG

54

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 323 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATTGTTT GTTGTTCAT TTTTTCTAA TGTCTCCCCT CTACCAGCTC	60
ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTTGC TCTCTGCTCA	120
TTCTCTCTGA AGTCTAGGTT ACCCATTGG GGGACCCATT ATAGGCAATA AACACAGTTC	180
CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTTCCTTT TCTTAGCCTT	240
TTCCTGCAAA AGGCTCACTC AGTCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT	300
AGGCTGCCTT CTTTTCCATG TCC	323

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 192 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATT TTAAATATCA CTTTGTATC ACTCTGACTT TTTAGCATAAC	60
TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTCACTC	120
TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTTCAT TTCCTTCACG TTGGCCAATG	180
GATAAACAAA GT	192

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTTA	TGGAATGAGT	AGACTGTATG	TTTGAANATT	TANCCACAAAC	CTCTTGACA	60
TATAATGACG	CAACAAAAAG	GTGCTGTTA	GTCCTATGGT	TCAGTTATG	CCCCTGACAA	120
GTTTCCATTG	TGTTTGCCG	ATCTTCTGGC	TAATCGTGGT	ATCCTCCATG	TTATTAGTAA	180
TTCTGTATTC	CATTTGTTA	ACGCCTGGTA	GATGTAACCT	GCTANGAGGC	TAACTTTATA	240
CTTATTTAAA	AGCTCTTATT	TTGTGGTCAT	TAAAATGGCA	ATTATGTGC	AGCACTTTAT	300
TGCAGCAGGA	AGCACGTGTG	GGTTGGTTGT	AAAGCTCTT	GCTAATCTTA	AAAAGTAATG	360
GG						362

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTGAAA	GATCGTGTCC	ACTCCTGTGG	ACATCTTGT	TTAATGGAGT	TTCCCATGCA	60
GTANGACTGG	TATGGTTGCA	GCTGTCCAGA	TAAAAACATT	TGAAGAGCTC	CAAAATGAGA	120
GTTCTCCCAG	GTTCGCCCTG	CTGCTCCAAG	TCTCAGCAGC	AGCCTCTTT	AGGAGGCATC	180
TTCTGAACTA	GATTAAGGCA	GCTTGTAAAT	CTGATGTGAT	TTGGTTTATT	ATCCAACCTAA	240
CTTCCATCTG	TTATCACTGG	AGAAAGCCCA	GACTCCCCAN	GACNGGTACG	GATTGTGGGC	300
ATANAAGGAT	TGGGTGAAGC	TGGCGTTGTG	GT			332

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ACTTTTGCCA	TTTTGTATAT	ATAAACAAATC	TTGGGACATT	CTCCTGAAAA	CTAGGTGTCC	60
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AGTGGCTAAG AGAACTCGAT TTCAAGCAAT TCTGAAAGGA AAACCAGCAT GACACAGAAT	120
CTCAAATTCC CAAACAGGGG CTCTGTGGGA AAAATGAGGG AGGACCTTG TATCTCGGGT	180
TTTAGCAAGT TAAAATGAAN ATGACAGGAA AGGCTTATTG ATCAACAAAG AGAAGAGTTG	240
GGATGCTTCT AAAAAAAACT TTGGTAGAGA AAATAGGAAT GCTNAATCCT AGGGAAGCCT	300
GTAACAATCT ACAATTGGTC CA	322

## (2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 278 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ACAAGCCTTC ACAAGTTAA CTAAATTGGG ATTAATCTTT CTGTANTTAT CTGCATAATT	60
CTTGTTCCTC TTTCCATCTG GCTCCTGGGT TGACAATTG TGGAAACAAAC TCTATTGCTA	120
CTATTAAAAA AAAATCACAA ATCTTCCCT TTAAGCTATG TTNAATTCAA ACTATTCCCTG	180
CTATTCCCTGT TTTGTCAAAG AAATTATATT TTTCAAAATA TGTNTATTG TTTGATGGGT	240
CCCACGAAAC ACTAATAAAA ACCACAGAGA CCAGCCTG	278

## (2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 121 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTTTANAAAAA CTTGTTTAGC TCCATAGAGG AAAGAATGTT AAACTTGTA TTTTAAAACA	60
TGATTCTCTG AGGTTAAACT TGGTTTTCAA ATGTTATTGTT TACTTGTATT TTGCTTTGG	120
T	121

## (2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 350 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACTTANAACC	ATGCCTAGCA	CATCAGAATC	CCTCAAAGAA	CATCAGTATA	ATCCTATACC	60
ATANCAAGTG	GTGACTGGTT	AAGCGTGCAG	CAAAGGTAG	CTGGCACATT	ACTTGTGTGC	120
AAAACCTGATA	CTTTTGTCT	AAGTAGGAAC	TAGTATACAG	TNCCTAGGAN	TGGTACTCCA	180
GGGTGCCCGCC	CAACTCCTGC	AGCCGCTCCT	CTGTGCCAGN	CCCTGNAAGG	AACTTTCGCT	240
CCACCTCAAT	CAAGCCCTGG	GCCATGCTAC	CTGCAATTGG	CTGAACAAAC	GTTCGCTGAG	300
TTCCCAAGGA	TGCAAAGCCT	GGTGCTAAC	TCCTGGGGCG	TCAACTCAGT		350

## (2) INFORMATION FOR SEQ ID NO:136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TGTACCGTGA	AGACGACAGA	AGTTGCATGG	CAGGGACAGG	GCAGGGCCGA	GGCCAGGGTT	60
GCTGTGATTG	TATCCGAATA	NTCCTCGTGA	GAAAAGATAA	TGAGATGACG	TGAGCAGCCT	120
GCAGACTTGT	GTCTGCCTTC	AANAAGCCAG	ACAGGAAGGC	CCTGCCTGCC	TTGGCTCTGA	180
CCTGGGGGCC	AGCCAGCCAG	CCACAGGTGG	GCTTCTTCCT	TTTGTGGTGA	CAACNCCAAG	240
AAAACCTGCAG	AGGCCAGGG	TCAGGTGTNA	GTGGGTANGT	GACCATAAAA	CACCAGGTGC	300
TCCCAGGAAC	CCGGGCAAAG	GCCATCCCCA	CCTACAGCCA	GCATGCCAC	TGGCGTGATG	360
GGTGCAGANG	GATGAAGCAG	CCAGNTGTT	TGCTGTGGT			399

## (2) INFORMATION FOR SEQ ID NO:137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACTGGTGTGG	TNGGGGGTGA	TGCTGGTGGT	ANAAAGTTGAN	GTGACTTCAN	GATGGTGTGT	60
GGAGGAAAGTG	TGTGAACGTA	GGGATGTAGA	NGTTTG GCC	GTGCTAAATG	AGCTTCGGGA	120
TTGGCTGGTC	CCACTGGTGG	TCACTGTCAT	TGGTGGGGTT	CCTGT		165

## (2) INFORMATION FOR SEQ ID NO:138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ACTCACTGGA	ATGCCACATT	CACAACAGAA	TCAGAGGTCT	GTGAAAACAT	TAATGGCTCC	60
TTAACCTCTC	CAGTAAGAAT	CAGGGACTTG	AAATGGAAAC	GTAAACAGCC	ACATGCCAA	120
TGCTGGGCAG	TCTCCCATGC	CTTCCACAGT	GAAAGGGCTT	GAGAAAAATC	ACATCCAATG	180
TCATGTGTTT	CCAGCCACAC	CAAAGGTGC	TTGGGGTGG	GGGCTGGGG	CATANANGT	240
CANGCCTCAG	GAAGCCTCAA	GTTCCATTCA	GCTTGCCAC	TGTACATTCC	CCATNTTTAA	300
AAAAACTGAT	GCCTTTTTT	TTTTTTTTG	TAAAATTC			338

- (2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 382 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGAATCTTG	GTTTTGGCA	TCTGGTTGC	CTATAGCCGA	GGCCACTTG	ACAGAACAAA	60
GAAAGGGACT	TCGAGTAAGA	AGGTGATT	CAGCCAGCCT	AGTGCCGAA	GTGAAGGAGA	120
ATTCAAACAG	ACCTCGTCAT	TCCTGGTGTG	AGCCTGGTCG	GCTCACCGCC	TATCATCTGC	180
ATTTGCCTTA	CTCAGGTGCT	ACCGGACTCT	GGCCCCTGAT	GTCTGTAGTT	TCACAGGATG	240
CCTTATTTGT	CTTCTACACC	CCACAGGGCC	CCCTACTTCT	TCGGATGTGT	TTTTAATAAT	300
GTCAGCTATG	TGCCCATCC	TCCTTCATGC	CCTCCCTCCC	TTTCCTACCA	CTGCTGAGTG	360
GCCTGGAACT	TGTTAAAGT	GT				382

- (2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 200 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAANCTT	CTTTCTGTTG	TGTTNGATT	TACTATAGGG	GTTTNGCTTN	TTCTAAANAT	60
ACTTTTCATT	TAACANCTT	TGTTAAGTGT	CAGGCTGCAC	TTTGCTCCAT	ANAATTATTG	120
TTTCACATT	TCAACTTGTA	TGTGTTGTC	TCTTANAGCA	TTGGTGAAAT	CACATATT	180
ATATTCA	TAAAGGAGAA					200

## (2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ACTTTATTTT CAAAACACTC ATATGTTGCA AAAAACACAT AGAAAAATAA AGTTTGGTGG	60
GGGTGCTGAC TAAACTTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTTGT	120
ATGCATGTAG AGAACCCAAA CTAATTATT AAACAGGATA GAAACAGGCT GTCTGGGTGA	180
AATGGTTCTG AGAACCATCC AATTACCTG TCAGATGCTG ATANACTAGC TCTTCAGATG	240
TTTTTCTACC AGTCAGAGA TNGGTTAATG ACTANTCCA ATGGGGAAAA AGCAAGATGG	300
ATTCACAAAC CAAGTAATT TAAACAAAGA CACTT	335

## (2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ACCAGGTTAA TATTGCCACA TATATCCTTT CCAATTGCGG GCTAAACAGA CGTGTATT	60
GGGTTGTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTT CATGGAGTAT	120
CTGATGGAGA AAACACTGAG TTTGACAAA TCTTATT	180
TTCAAACATC ATAGCCAATG ATGCCCGCT TGCCTATAAT CTCTCCGACA TAAAACCACA	240
TCAACACCTC AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACTGTG AGCTGTTGA	300
AGCTACCACT AGCTAACCT TGGACTATNT TTTCANGCT CTGAATAGCT CTAGGGATCT	360
CAGCANGGT GGGAGGAACC AGCTAACCT TGGCGTANT	420
	459

## (2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

ACATTCCTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG	60
AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTACCA ACCCCACCCA TCTCCCTGAG	120
ACCATCCGAC TTCCCTGTGT	140

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACTTCAGTAA CAACATACAA TAACAAACATT AAGTGTATAT TGCCATCTTT GTCATTTCT	60
ATCTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTG	120
AGGCAATTAA TCCATATTG TTTTCAATAA GGAAAAAAAG ATGT	164

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ACGTAGACCA TCCAACTTTG TATTTGTAAT GGCAAACATC CAGNAGCAAT TCCTAAACAA	60
ACTGGAGGGT ATTTATACCC AATTATCCCA TTCATTAACA TGCCCTCCTC CTCAGGCTAT	120
GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTGAT ATAAACTTCA	180
GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGAG GAAATGGAAC ATAAGCCCAG	240
TAGTAAAATN TTGCTTAGCT GAAACAGCCA CAAAGACTT ACCGCCGTGG TGATTACCAT	300
CAA	303

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACTGCAGCTC	AATTAGAAGT	GGTCTCTGAC	TTTCATCANC	TTCTCCCTGG	GCTCCATGAC	60
ACTGGCCTGG	AGTGACTCAT	TGCTCTGGTT	GGTTGAGAGA	GCTCCTTGC	CAACAGGCCT	120
CCAAGTCAGG	GCTGGGATT	GTTTCCTTTC	CACATTCTAG	CAACAATATG	CTGGCCACTT	180
CCTGAACAGG	GAGGGTGGGA	GGAGCCAGCA	TGGAACAAGC	TGCCACTTTC	TAAAGTAGCC	240
AGACTTGC	CTGGGCCTGT	CACACCTACT	GATGACCTTC	TGTGCCTGCA	GGATGGAATG	300
TTAGGGTGAG	CTGTGTGACT	CTATGGT				327

## (2) INFORMATION FOR SEQ ID NO:147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACATTGTTT	TTTGAGATAA	AGCATTGANA	GAGCTCTCCT	TAACGTGACA	CAATGGAAGG	60
ACTGGAACAC	ATACCCACAT	CTTTGTTCTG	AGGGATAATT	TTCTGATAAA	GTCTTGCTGT	120
ATATTCAAGC	ACATATGTTA	TATATTATTC	AGTTCCATGT	TTATAGCCTA	GTT	173

## (2) INFORMATION FOR SEQ ID NO:148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACAACCAC	TATCTCATCG	AATTTTAAC	CCAAACTCAC	TCACTGTGCC	TTTCTATCCT	60
ATGGGATATA	TTATTTGATG	CTCCATTCA	TCACACATAT	ATGAATAATA	CACTCATACT	120
GCCCTACTAC	CTGCTGCAAT	AATCACATT	CCTTCCTGTC	CTGACCCCTGA	AGCCATTGGG	180
GTGGTCTTAG	TGGCCATCAG	TCCANGCCTG	CACCTTGAGC	CCTTGAGCTC	CATTGCTCAC	240
NCCANCCCAC	CTCACCGACC	CCATCCTCTT	ACACAGCTAC	CTCCTTGCTC	TCTAACCCCA	300
TAGATTATNT	CCAAATTCA	TCAATTAAGT	TACTATTAAC	ACTCTACCCG	ACATGTCCAG	360
CACCACTGGT	AAGCCTTCTC	CAGCCAACAC	ACACACACAC	ACACNCACAC	ACACACATAT	420
CCAGGCACAG	GCTACCTCAT	CTTCACAATC	ACCCCTTAA	TTACCATGCT	ATGGTGG	477

## (2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTAAAG AGGGAAGAAC	60
TAACGTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGAG TGGATGTAA GGTGGGCCT	120
GATGATAAAAT AAGAGTCAGC CAGGTAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAACAA	180
TTTCAGGCAG AGGAAACAGC AGTGAAA	207

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG	60
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTGCG T	111

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCGCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC	60
AGCAAGATGG CTTTGAACTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAC	120
GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCCACTG TGGTCCCCAC TGTCTACGAG	180
GTGCATCCGG CTCAGT	196

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC	60
CTTCCCCTTT TCATCTAGTG GTGGAAACCT GATGCTTTAT GTTGACAGGA ATAGAACCGAG	120
GAGGGAGTTT GT	132

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACAANACCCA NGANAGGCCA CTGGCCGTGG TGTATGGCC TCCAAACATG AAAGTGTCAAG	60
CTTCTGCTCT TATGTCCTCA TCTGACAACCT CTTTACCAATT TTTATCCTCG CTCAGCAGGA	120
GCACATCAAT AAAGTCCAAA GTCTTGGACT TGGCCTTGCG TTGGAGGAAG TCATCAACAC	180
CCTGGCTAGT GAGGGTGCAG CGCCGCTCCT GGATGACGGC ATCTGTGAAG TCGTGCACCA	240
GTCTGCAGGC CCTGTGGAAG CGCCGTCCAC ACGGAGTNAG GAATT	285

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACCACAGTCC TGTTGGGCCA GGGCTTCATG ACCCTTTCTG TGAAAAGCCA TATTATCACC	60
ACCCCAAATT TTTCCCTTAAA TATCTTTAAC TGAAGGGGTC AGCCTCTTGA CTGCAAAGAC	120
CCTAACGCCGG TTACACAGCT AACTCCCACCT GGCCCTGATT TGTGAAATTG CTGCTGCCTG	180
ATTGGCACAG GAGTCGAAGG TGTTCAAGCTC CCCTCCTCCG TGGAACGAGA CTCTGATTG	240
AGTTTCACAA ATTCTCGGGC CACCTCGTCA TTGCTCCTCT GAAATAAAAT CCGGAGAATG	300

GTCAGGCCTG TCTCATCCAT ATGGATCTTC CGG

333

## (2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 308 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAAA GATCATCAGG GCATGGATGG	60
GAAAGTGCTT TGGGAACGTG AAAGTGCCTA ACACATGATC GATGATTTTT GTTATAATAT	120
TTGAATCACG GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGGCCCCAG CCCCAGCCCC	180
ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTGGCT	240
GCTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGTAGGCATGCTG	300
GCCCTGGT	308

## (2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 295 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGAA CATATTAGGA ACTCAAAATA TGAGATGATA ACAGTGCCTA	60
TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAACTGA	120
GAATAGGAGA TTATGTTGG CCCTCATATT CTCTCCTATC CTCCTTGCT CATTCTATGT	180
CTAATATATT CTCAATCAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT	240
AAAACCAGAT GTCTATCCTT AAGATTTCA AATAGAAAAC AAATTAACAG ACTAT	295

## (2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAGTTAA ATAGTGCTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTTCT	60
GAAGAGCAAA ACAAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGGT A TATCTGTCCC	120
CTTAGT	126

## (2) INFORMATION FOR SEQ ID NO:158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ACCCACTGGT CTTGGAAACA CCCATCCTTA ATACGATGAT TTTCTGTCG TGTGAAAATG	60
AANCCAGCAG GCTGCCCTA GTCAGTCCTT CCTTCCAGAG AAAAAGAGAT TTGAGAAAGT	120
GCCTGGGTAA TTCACCATTA ATTCCTCCC CCAAACCTCTC TGAGTCTTCC CTTAATATT	180
CTGGTGGTTC TGACCAAAGC AGGTCACTGGT TTGTTGAGCA TTTGGGATCC CAGTGAAGTA	240
NATGTTGTA GCCTTGCATA CTTAGCCCTT CCCACGCACA AACGGAGTGG CAGAGTGGTG	300
CCAACCCTGT TTTCCCAGTC CACGTAGACA GATTCACAGT GCGGAATTCT GGAAGCTGGA	360
NACAGACGGG CTCTTGCAG AGCCGGGACT CTGAGANGGA CATGAGGGCC TCTGCCTCTG	420
TGTTCATTCT CTGATGTCCT GT	442

## (2) INFORMATION FOR SEQ ID NO:159:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

ACTTCCAGGT AACGTTGTTG TTTCCGTTGA GCCTGAAGTG ATGGGTGACG TTGTAGGTT	60
TCCAACAAGA ACTGAGGTTG CAGAGCGGGT AGGGAAGAGT GCTGTTCCAG TTGCACCTGG	120
GCTGCTGTGG ACTGTTGTTG ATTCCCTCACT ACGGCCAAG GTTGTGGAAC TGGCANAAAG	180
GTGTGTTGTT GGANTTGAGC TCGGGCGGCT GTGGTAGGTT GTGGGCTCTT CAACAGGGC	240
TGCTGTGGTG CCGGGANGTG AANGTGTGTT GTCACTTGAG CTTGGCCAGC TCTGGAAAGT	300
ANTANATTCT TCCTGAAGGC CAGCGCTTGT GGAGCTGGCA NGGGTCANTG TTGTGTGTA	360
CGAACCCAGTG CTGCTGTGGG TGGGTGTANA TCCTCCACAA AGCCTGAAGT TATGGTGTCA	420
TCAGGTAANA ATGTGGTTTC AGTGTCCCTG GGCGNGCTGTG GAAGGTTGTA NATTGTCACC	480
AAGGGAATAA GCTGTGGT	498

## (2) INFORMATION FOR SEQ ID NO:160:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ACCTGCATCC	AGCTTCCCTG	CCAAACTCAC	AAGGAGACAT	CAACCTCTAG	ACAGGGAAAC	60
AGCTTCAGGA	TACTTCCAGG	AGACAGAGCC	ACCAGCAGCA	AAACAAATAT	TCCCATGCCT	120
GGAGCATGGC	ATAGAGGAAG	CTGANAAATG	TGGGGTCTGA	GGAAGCCATT	TGAGTCTGGC	180
CACTAGACAT	CTCATCAGCC	ACTTGTGTGA	AGAGATGCC	CATGACCCCA	GATGCCTCTC	240
CCACCCTTAC	CTCCATCTCA	CACACTTGAG	CTTTCCACTC	TGTATAATT	TAACATCCTG	300
GAGAAAAATG	GCAGTTGAC	CGAACCTGTT	CACAAACGGTA	GAGGCTGATT	TCTAACGAAA	360
CTTGTAGAAT	GAAGCCTGGA					380

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 114 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ACTCCACATC	CCCTCTGAGC	AGGCGGTTGT	CGTTCAAGGT	GTATTGGCC	TTGCCTGTCA	60
CACTGTCCAC	TGGCCCTTA	TCCACTTGGT	GCTTAATCCC	TCGAAAGAGC	ATGT	114

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ACTTTCTGAA	TCGAATCAA	TGATACTTAG	TGTAGTTTA	ATATCCTCAT	ATATATCAA	60
GTTTTACTAC	TCTGATAATT	TTGTAAACCA	GGTAACCAGA	ACATCCAGTC	ATACAGCTT	120
TGGTGATATA	TAACTTGGCA	ATAACCCAGT	CTGGTGATAC	ATAAAACTAC	TCACTGT	177

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTATACA GACAGGGGTG AAGACATTCA CGACAAAAAC GCGAAATTCT ATCCCGTGAC	60
CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT	120
CATCAGCGGC ATGATGT	137

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTTA	60
TGCAATGCAT CATGCTATTT CATACTAAT GAGGGAGTTC CAGGAGATTG AACCAGGAAA	120
TGCATGGATC TCAAAGGAAA CAAACACCCA ATAAACTCGG AGTGGCAGAC TGACAACTGT	180
GAGACATGCA CTTGCTACGA AACAGAAATT TCATGTTGCA CCCTTGTTC TACACCTGTG	240
GGTTATGACA AAGACAAC TG CCAAAGAATC TTCAAGAAGG AGGACTGCAA GTATATCGTG	300
GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCAGTG AATGGATAAT CTAATGTGCT	360
TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT	420
GATTGTGTAG CCATGCCTAT CAGTAAAAAG ATNTTGAGC AAACACTTT	469

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ACAGTTTTT ATANATATCG ACATTGCCGG CACTTGTGTT CAGTTTCATA AAGCTGGTGG	60
------------------------------------------------------------------	----

ATCCGCTGTC ATCCACTATT CCTTGGCTAG AGTAAAAATT ATTCTTATAG CCCATGTCCC	120
TGCAGGCCGC CCGCCCGTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT	180
TCCTCTGAGA TGAGT	195

## (2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACATCTTAGT AGTGTGGCAC ATCAGGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC	60
CGAGGGTCGGA GTCCACACCA CCGGTGTAAG TGTGCTCAAT CTTGGGCTTG GCGCCCACCT	120
TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAACTCG CCAAAGAATT	180
TTTGCAGACC AGCCTGAGCA AGGGGGCGGAT GTTCAGCTTC AGCTCCTCCT TCGTCAGGTG	240
GATGCCAACC TCGTCTANGG TCCGTGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGC	300
GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCCACGAAA CTTCTCTGGG AGCTGCTAGT	360
NGGGGCCTTT TTGGTGAAC TTTC	383

## (2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 247 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT	60
TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC	120
TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC	180
TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC	240
TGANGTC	247

## (2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 273 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACTTCTAAGT	TTTCTAGAAG	TGGAAGGATT	GTANTCATCC	TGAAAATGGG	TTTACTTCAA	60
AATCCCTCAN	CCTTGTCTT	CACNACTGTC	TATACTGANA	GTGTCATGTT	TCCACAAAGG	120
GCTGACACCT	GAGCCTGNAT	TTTCACTCAT	CCCTGAGAAG	CCCTTCCAG	TAGGGTGGGC	180
AATTCCCAAC	TTCCTTGCCA	CAAGCTTCCC	AGGCTTCTC	CCCTGGAAA	CTCCAGCTTG	240
AGTCCAGAT	ACACTCATGG	GCTGCCCTGG	GCA			273

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACAGCCTTGG	CTTCCCCAAA	CTCCACAGTC	TCAGTGCAGA	AAGATCATCT	TCCAGCAGTC	60
AGCTCAGACC	AGGGTCAAAG	GATGTGACAT	CAACAGTTTC	TGGTTTCAGA	ACAGGTTCTA	120
CTACTGTCAA	ATGACCCCCC	ATACTTCCTC	AAAGGCTGTG	GTAAGTTTG	CACAGGTGAG	180
GGCAGCAGAA	AGGGGGTANT	TACTGATGGA	CACCATCTTC	TCTGTATACT	CCACACTGAC	240
CTTGCCATGG	GCAAAGGCC	CTACCACAAA	AACAATAGGA	TCACTGCTGG	GCACCAGCTC	300
ACGCACATCA	CTGACAACCG	GGATGGAAA	AGAANTGCCA	ACTTCATAC	ATCCAACCTGG	360
AAAGTGATCT	GATACTGGAT	TCTTAATTAC	CTTAAAAGC	TTCTGGGGC	CATCAGCTGC	420
TCGAACACTG	A					431

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC	TGGGCTGTTA	TGCCTGTGCC	GGCTGCTGAA	AGGGAGTTCA	GAGGTGGAGC	60
TCAAGGAGCT	CTGCAGGCAT	TTTGCCAANC	CTCTCCANAG	CANAGGGAGC	AACCTACACT	120
CCCCGCTAGA	AAGACACCAAG	ATTGGAGTCC	TGGGAGGGGG	AGTTGGGGTG	GGCATTGAT	180
GTATACTTGT	CACCTGAATG	AANGAGCCAG	AGAGGAANGA	GACGAANATG	ANATTGGCCT	240
TCAAAGCTAG	GGGTCTGGCA	GGTGGGA				266

(2) INFORMATION FOR SEQ ID NO:171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GGCAGCCAAA	TCATAAACGG	CGAGGGACTGC	AGCCCGCACT	CGCAGCCCTG	GCAGGGCGGCA	60
CTGGTCATGG	AAAACGAATT	GTTCTGCTCG	GGCGTCCTGG	TGCATCCGCA	GTGGGTGCTG	120
TCAGCCGCAC	ACTGTTCCA	GAAGTGAGTG	CAGAGCTCCT	ACACCATCGG	GCTGGGCCTG	180
CACAGTCTTG	AGGCCGACCA	AGAGCCAGGG	AGCCAGATGG	TGGAGGCCAG	CCTCTCCGTA	240
CGGCACCCAG	AGTACAACAG	ACCCTTGCTC	GCTAACGACCC	TCATGCTCAT	CAAGTTGGAC	300
GAATCCGTGT	CCGAGTCTGA	CACCATCCGG	AGCATCAGCA	TTGCTTCGCA	GTGCCCTACC	360
GCGGGGAAC	CTTGCCTCGT	TTCTGGCTGG	GGTCTGCTGG	CGAACGGCAG	AATGCCTACC	420
GTGCTGCAGT	GCGTGAACGT	GTCGGTGGTG	TCTGAGGAGG	TCTGCAGTAA	GCTCTATGAC	480
CCGCTGTACC	ACCCCAGCAT	GTTCTGCGCC	GGCGGAGGGC	AAGACCAGAA	GGACTCCTGC	540
AACGGTGACT	CTGGGGGGCC	CCTGATCTGC	AACGGGTACT	TGCAGGGCCT	TGTGTCTTTC	600
GGAAAAGCCC	CGTGTGGCCA	AGTTGGCGTG	CCAGGTGTCT	ACACCAACCT	CTGCAAATTC	660
ACTGAGTGGA	TAGAGAAAAC	CGTCCAGGCC	AGTTAACTCT	GGGGACTGGG	AACCCATGAA	720
ATTGACCCCC	AAATACATCC	TGCGGAAGGA	ATTCAAGGAAT	ATCTGTTCCC	AGCCCCTCCT	780
CCCTCAGGCC	CAGGAGTCCA	GGCCCCCAGC	CCCTCCTCCC	TCAAACCAAG	GGTACAGATC	840
CCCAGCCCC	CCTCCCTCAG	ACCCAGGAGT	CCAGACCCCC	CAGCCCCCTCC	TCCCTCAGAC	900
CCAGGAGTCC	AGCCCCTCCT	CCCTCAGACC	CAGGAGTCCA	GACCCCCCAG	CCCCTCCTCC	960
CTCAGACCCA	GGGGTCCAGG	CCCCCAACCC	CTCCTCCCTC	AGACTCAGAG	GTCCAAGCCC	1020
CCAACCCNTC	ATTCCCCAGA	CCCAGAGGTC	CAGGTCCCAG	CCCCTCNTCC	CTCAGACCCA	1080
GCGGTCCAAT	GCCACCTAGA	CTNTCCCTGT	ACACAGTGCC	CCCTTGTGGC	ACGTTGACCC	1140
AACCTTACCA	GTTGGTTTTT	CATTTTNGT	CCCTTTCCCC	TAGATCCAGA	AATAAAGTTT	1200
AAGAGAAGNG	CAAAAAAAA	AAAAAAA	AAAAAAA	AAAAAAA	AAAAAAA	1248

(2) INFORMATION FOR SEQ ID NO:172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met	Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro
1															15

Leu	Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser
20															30

Glu	Ser	Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45	
Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly			
50	55	60	
Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu			
65	70	75	80
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe			
85	90	95	
Cys Ala Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser			
100	105	110	
Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe			
115	120	125	
Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn			
130	135	140	
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser			
145	150	155	

## (2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1265 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCAGCCCGC ACTCGCAGCC CTGGCAGGCG GCACTGGTCA TGGAAAACGA ATTGTTCTGC	60
TCGGCGTCC TGGTGCATCC GCAGTGGGTG CTGTCAGCCG CACACTGTT CCAGAACTCC	120
TACACCATCG GGCTGGGCCT GCACAGTCTT GAGGCCGACC AAGAGCCAGG GAGCCAGATG	180
GTGGAGGCCA GCCTCTCCGT ACGGCACCCA GAGTACAACA GACCCTTGCT CGCTAACGAC	240
CTCATGCTCA TCAAGTTGGA CGAATCCGTG TCCGAGTCTG ACACCATCCG GAGCATCAGC	300
ATTGCTTCGC AGTGCCCTAC CGCGGGGAAC TCTTGCCTCG TTTCTGGCTG GGGTCTGCTG	360
GCGAACGGTG AGCTCACGGG TGTGTGTCTG CCCTCTTCAA GGAGGTCCTC TGCCCAGTCG	420
CGGGGGCTGA CCCAGAGCTC TGCCTCCCAG GCAGAACGCC TACCGTGCTG CAGTGCCTGA	480
ACGTGTCGGT GGTGTCTGAG GAGGTCTGCA GTAAGCTCTA TGACCCGCTG TACCACCCCA	540
GCATGTTCTG CGCCGGCGGA GGGCAAGACC AGAAGGACTC CTGCAACGGT GACTCTGGGG	600
GGCCCCTGAT CTGCAACGGG TACTTGCAGG GCCTTGTGTC TTTCGGAAAA GCCCCGTGTG	660
GCCAAGTTGG CGTGCCAGGT GTCTACACCA ACCTCTGCAA ATTCACTGAG TGGATAGAGA	720
AAACCGTCCA GGCCAGTTAA CTCTGGGAC TGGGAACCCA TGAAATTGAC CCCCAAATAC	780
ATCCTGCGGA AGGAATTCTAG GAATATCTGT TCCCAGCCCC TCCTCCCTCA GGCCCAGGAG	840
TCCAGGCCCC CAGCCCCTCC TCCCTCAAAC CAAGGGTACA GATCCCCAGC CCCTCCTCCC	900
TCAGACCCAG GAGTCCAGAC CCCCCAGCCC CTCCTCCCTC AGACCCAGGA GTCCAGCCCC	960
TCCTCCNTCA GACCCAGGAG TCCAGACCCC CCAGCCCCCTC CTCCCTCAGA CCCAGGGGTT	1020
GAGGCCCCCA ACCCCTCCTC CTTCAAGAGTC AGAGGTCCAA GCCCCCCAAC CCTCGTTCCC	1080
CAGACCCAGA GGTNNAGGTC CCAGCCCCTC TTCCNTCAGA CCCAGNGGTC CAATGCCACC	1140
TAGATTTCC CTGNACACAG TGCCCCCTTG TGGNANGTTG ACCCAACCTT ACCAGTTGGT	1200

TTTCATTT TNGTCCCTTT CCCCTAGATC CAGAAATAAA GTTTAAGAGA NGNGAAAAAA	1260
AAAAAA	1265

## (2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1459 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGTCAGCCGC	ACACTGTTTC	CAGAAGTGAG	TGCAGAGCTC	CTACACCATC	GGGCTGGGCC	60
TGCACAGTCT	TGAGGCCGAC	CAAGAGCCAG	GGAGCCAGAT	GGTGGAGGCC	AGCCTCTCCG	120
TACGGCACCC	AGAGTACAAC	AGACCCTTGC	TCGCTAACGA	CCTCATGCTC	ATCAAGTTGG	180
ACGAATCCGT	GTCCGAGTCT	GACACCATCC	GGAGCATCAG	CATTGCTTCG	CAGTGCCCTA	240
CCGCGGGGAA	CTCTTGCCTC	GTTCCTGGCT	GGGGTCTGCT	GGCGAACGGT	GAGCTCACGG	300
GTGTGTGTCT	GCCCTCTTCA	AGGAGGTCTC	CTGCCAGTC	GCGGGGGCTG	ACCCAGAGCT	360
CTGCGTCCCA	GGCAGAATGC	CTACCGTGCT	GCAGTGCCTG	AACGTGTCGG	TGGTGTCTGA	420
NGAGGTCTGC	ANTAAAGCTCT	ATGACCCGCT	GTACCACCCC	ANCATGTTCT	GCGCCGGCGG	480
AGGGCAAGAC	CAGAAGGACT	CCTGCAACGT	GAGAGAGGGG	AAAGGGGAGG	GCAGGCGACT	540
CAGGGAAAGGG	TGGAGAAGGG	GGAGACAGAG	ACACACAGGG	CCGCATGGCG	AGATGCAGAG	600
ATGGAGAGAC	ACACAGGGAG	ACAGTGACAA	CTAGAGAGAG	AAACTGAGAG	AAACAGAGAA	660
ATAAACACAG	GAATAAAGAG	AAGCAAAGGA	AGAGAGAAAC	AGAAACAGAC	ATGGGGAGGC	720
AGAAACACAC	ACACATAGAA	ATGCAGTTGA	CCTTCCAACA	GCATGGGGCC	TGAGGGCGGT	780
GACCTCCACC	CAATAGAAAA	TCCTCTTATA	ACTTTGACT	CCCCAAAAAC	CTGACTAGAA	840
ATAGCCTACT	GTTGACGGGG	AGCCTTACCA	ATAACATAAA	TAGTCGATT	ATGCATACGT	900
TTTATGCATT	CATGATATAC	CTTTGTTGGA	ATTTTTGAT	ATTTCTAACG	TACACAGTTC	960
GTCTGTGAAT	TTTTTAAAT	TGTTGCAACT	CTCCTAAAAT	TTTTCTGATG	TGTTTATTGA	1020
AAAAATCCAA	GTATAAGTGG	ACTTGTGCAT	TCAAACCAGG	GTTGTTCAAG	GGTCAACTGT	1080
GTACCCAGAG	GGAAACAGTG	ACACAGATT	ATAGAGGTGA	AACACGAAGA	GAAACAGGAA	1140
AAATCAAGAC	TCTACAAAGA	GGCTGGGCAG	GGTGGCTCAT	GCCTGTAATC	CCAGCACTTT	1200
GGGAGGCGAG	GCAGGCCAGAT	CACTTGAGGT	AAGGAGTTCA	AGACCAGCCT	GGCCAAAATG	1260
GTGAAATCCT	GTCTGTACTA	AAAATACAAA	AGTTAGCTGG	ATATGGTGGC	AGGCGCCTGT	1320
AATCCCAGCT	ACTTGGGAGG	CTGAGGCAGG	AGAATTGCTT	GAATATGGGA	GGCAGAGGTT	1380
GAAGTGAGTT	GAGATCACAC	CACTATACTC	CAGCTGGGGC	AACAGAGTAA	GACTCTGTCT	1440
CAAAAAAA	AAAAAAA					1459

## (2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1167 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GCGCAGCCCT	GGCAGGCGGC	ACTGGTCATG	GAAAACGAAT	TGTTCTGCTC	GGCGTCCTG	60
GTGCATCCGC	AGTGGGTGCT	GTCAGCCGCA	CACTGTTCC	AGAACTCCTA	CACCATCGGG	120
CTGGGCCTGC	ACAGTCTTGA	GGCCGACCAA	GAGCCAGGGA	GCCAGATGGT	GGAGGCCAGC	180
CTCTCCGTAC	GGCACCCAGA	GTACAACAGA	CTCTGCTCG	CTAACGACCT	CATGCTCATC	240
AAGTTGGACG	AATCCGTGTC	CGAGTCTGAC	ACCATCCGGA	GCATCAGCAT	TGCTTCGCAG	300
TGCCCTACCG	CGGGGAACTC	TTGCCTCGTN	TCTGGCTGGG	GTCTGCTGGC	GAACGGCAGA	360
ATGCCTACCG	TGCTGCACTG	CGTGAACGTG	TCGGTGGTGT	CTGAGGANGT	CTGCAGTAAG	420
CTCTATGACC	CGCTGTACCA	CCCCAGCATG	TTCTGCGCCG	GGGGAGGGCA	AGACCAGAAG	480
GAECTCCTGCA	ACGGTGACTC	TGGGGGGCCC	CTGATCTGCA	ACGGGTACTT	GCAGGGCCTT	540
GTGTCTTCG	GAAAAGCCCC	GTGTGGCCAA	CTTGGCGTGC	CAGGTGTCTA	CACCAACCTC	600
TGCAAATTCA	CTGAGTGGAT	AGAGAAAACC	GTCCAGNCCA	GTAACTCTG	GGGACTGGGA	660
ACCCATGAAA	TTGACCCCCA	AATACATCCT	GCAGGAANGAA	TTCAGGAATA	TCTGTTCCA	720
GCCCCTCCTC	CCTCAGGCC	AGGAGTCCAG	GCCCCCAGCC	CCTCCTCCCT	CAAACCAAGG	780
GTACAGATCC	CCAGCCCCTC	CTCCCTCAGA	CCCAGGAGTC	CAGACCCCCC	AGCCCCCTCNT	840
CCNTCAGACC	CAGGAGTCCA	GCCCCCTCCTC	CNTCAGACGC	AGGAGTCCAG	ACCCCCCAGC	900
CCNTCNTCCG	TCAGACCCAG	GGGTGCAGGC	CCCCAACCCC	TCNTCCNTCA	GAGTCAGAGG	960
TCCAAGCCCC	CAACCCCTCG	TTCCCCAGAC	CCAGAGGTNC	AGGTCCCAGC	CCCTCCTCCC	1020
TCAGACCCAG	CGGTCCAATG	CCACCTAGAN	TNTCCCTGTA	CACAGTGCC	CCTTGTGGCA	1080
NGTTGACCCA	ACCTTACCAAG	TTGGTTTTTC	ATTTTTGTC	CCTTCCCCT	AGATCCAGAA	1140
ATAAAGTNTA	AGAGAAGCGC	AAAAAAA				1167

## (2) INFORMATION FOR SEQ ID NO:176:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1				5					10						15
Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
					20				25						30
Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
				35			40							45	
Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Leu	Leu	
					50		55							60	
Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu	Ser
					65		70			75					80
Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala	Gly
					85				90						95
Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly	Arg	Met
				100				105							110

Pro	Thr	Val	Leu	His	Cys	Val	Asn	Val	Ser	Val	Val	Ser	Glu	Xaa	Val
115							120							125	
Cys	Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met	Phe	Cys	Ala
130							135							140	
Gly	Gly	Gly	Gln	Asp	Gln	Lys	Asp	Ser	Cys	Asn	Gly	Asp	Ser	Gly	Gly
145							150							160	
Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe	Gly	Lys
	165							170						175	
Ala	Pro	Cys	Gly	Gln	Leu	Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn	Leu	Cys
	180							185						190	
Lys	Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Xaa	Ser			
	195						200							205	

## (2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1119 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GCGCACTCGC	AGCCCTGGCA	GGCGGCAGTG	GTCATGGAAA	ACGAATTGTT	CTGCTCGGGC	60
GTCCTGGTGC	ATCCGCAGTG	GGTGCTGTCA	GCCGCACACT	GTTTCCAGAA	CTCCTACACC	120
ATCGGGCTGG	GCCTGCACAG	TCTTGAGGCC	GACCAAGAGC	CAGGGAGCCA	GATGGTGGAG	180
GCCAGCCTCT	CCGTACGGCA	CCCAGAGTAC	AACAGACCCT	TGCTCGCTAA	CGACCTCATG	240
CTCATCAAGT	TGGACGAATC	CGTGTCCGAG	TCTGACACCA	TCCGGAGCAT	CAGCATTGCT	300
TCGCAGTGCC	CTACCGCGGG	GAACCTTGC	CTCGTTCTG	GCTGGGGTCT	GCTGGCGAAC	360
GATGCTGTGA	TTGCCATCCA	GTCCCAGACT	GTGGGAGGCT	GGGAGTGTGA	GAAGCTTTCC	420
CAACCCTGGC	AGGGTTGTAC	CATTCGGCA	ACTTCCAGTG	CAAGGACGTC	CTGCTGCATC	480
CTCACTGGGT	GCTCACTACT	GCTCACTGCA	TCACCCGGAA	CACTGTGATC	AACTAGCCAG	540
CACCATAGTT	CTCCGAAGTC	AGACTATCAT	GATTACTGTG	TTGACTGTGC	TGTCTATTGT	600
ACTAACCATG	CCGATGTTA	GGTGAAATTA	GCGTCACTTG	GCCTCAACCA	TCTTGGTATC	660
CAGTTATCCT	CACTGAATTG	AGATTCCCTG	CTTCAGTGTG	AGCCATTCCC	ACATAATTTC	720
TGACCTACAG	AGGTGAGGGA	TCATATAGCT	CTTCAAGGAT	GCTGGTACTC	CCCTCACAAA	780
TTCATTCTC	CTGTTGTAGT	GAAAGGTGCG	CCCTCTGGAG	CCTCCCAGGG	TGGGTGTGCA	840
GGTCACAATG	ATGAATGTAT	GATCGTGTTC	CCATTACCCA	AAGCCTTAA	ATCCCTCATG	900
CTCAGTACAC	CAGGGCAGGT	CTAGCATTTC	TTCATTTAGT	GTATGCTGTC	CATTCATGCA	960
ACCACCTCAG	GACTCCTGGA	TTCTCTGCCT	AGTTGAGCTC	CTGCATGCTG	CCTCCTTGGG	1020
GAGGTGAGGG	AGAGGGCCA	TGGTTCAATG	GGATCTGTGC	AGTTGTAACA	CATTAGGTGC	1080
TTAATAAACAA	GAAGCTGTGA	TGTTAAAAAA	AAAAAA			1119

## (2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 164 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1           5           10           15

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20          25           30

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35          40           45

Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
 50          55           60

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65          70           75           80

Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85          90           95

Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
100         105          110

Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
115         120          125

Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
130         135          140

Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
145         150          155          160

Pro Gly Thr Leu
  
```

## (2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```

CTGGAGTGCC TTGGTGTTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT 60
CCAGCTGCCCGGGG GATGCGAGGC TCGGAGCACC CTTGCCCGGC TGTGATTGCT 120
GCCAGGCACT GTTCATCTCA GCTTTCTGT CCCTTGCTC CCGGCAAGCG CTTCTGCTGA 180
AAGTCATAT CTGGAGCCTG ATGTCTTAAC GAATAAAGGT CCCATGCTCC ACCCGAAAAA 240
AAAAAAAAAAA 250
  
```

## (2) INFORMATION FOR SEQ ID NO:180:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCAA CACAATGGCT ACCTTTAAC	60
TCACCCAGAC CCCGCCCTG CCCGTGCCCC ACGCTGCTGC TAACGACAGT ATGATGCTTA	120
CTCTGCTACT CGGAAACTAT TTTTATGTAA TTAATGTATG CTTTCTTGTGTT TATAAATGCC	180
TGATTAAAAA AAAAAAAA AA	202

## (2) INFORMATION FOR SEQ ID NO:181:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTGKT NAGGTTKKG AGACAMCCCK AGACCTWAAN CTGTGTCACA GACTTCYNGG	60
AATGTTAGG CAGTGCTAGT AATTCYTCG TAATGATTCT GTTATTACTT TCCTNATTCT	120
TTATTCCTCT TTCTCTGAA GATTAATGAA GTTAAAATT GAGGTGGATA AATACAAAAAA	180
GGTAGTGTGA TAGTATAAGT ATCTAAGTGC AGATGAAAGT GTGTTATATA TATCCATTCA	240
AAATTATGCA AGTTAGTAAT TACTCAGGGT TAACTAAATT ACTTTAATAT GCTGTTGAAC	300
CTACTCTGTT CCTGGCTAG AAAAAATTAT AAACAGGACT TTGTTAGTT GGGAGCCAA	360
ATTGATAATA TTCTATGTT TAAAAGTTGG GCTATACATA AATTATTAAG AAATATGGAW	420
TTTTATTCCC AGGAATATGG KGTCATTT ATGAATATTA CSCRGGATAG AWGTWTGAGT	480
AAAAYCAGTT TTGGTWAATA YGTWAATATG TCMTAAATAA ACAAKGCTTT GACTTATTTC	540
CAAAAAAAA AAAAAAAA	558

## (2) INFORMATION FOR SEQ ID NO:182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTK GRGGATGCTA AGSCCCRGA RWTYGTTGA TCCAACCCTG GCTTWTTTC	60
AGAGGGGAAA ATGGGGCCTA GAAGTTACAG MSCATYTAGY TGGTGCGMTG GCACCCCTGG	120
CSTCACACAG ASTCCCGAGT AGCTGGACT ACAGGCACAC AGTCACTGAA GCAGGCCCTG	180
TTWGCAATTAC CGTTGCCAC CTCCAACCTTA AACATTCTTC ATATGTGATG TCCTTAGTCA	240
CTAAGGTTAA ACTTCCCAC CCAGAAAAGG CAACTTAGAT AAAATCTTAG AGTACTTTCA	300
TACTMTTCTA AGTCCTCTTC CAGCCTCACT KKGAGTCCTM CYTGGGGTT GATAGGAANT	360
NTCTCTTGGC TTTCTCAATA AARTCTCTAT YCATCTCATG TTTAATTGG TACGCATARA	420
AWTGSTGARA AAATAAAAAT GTTCTGGTTY MACTTTAAAA AAAAAAAA AAAAAAAA	479

## (2) INFORMATION FOR SEQ ID NO:183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AGGCAGGGAGC	AGAACGCTAAA	GCCAAAGCCC	AAGAACAGTG	GCAGTGCCAG	CACTGGTGCC	60
AGTACCAAGTA	CCAATAACAG	TGCCAGTGCC	AGTGCAGCA	CCAGTGGTGG	CTTCAGTGCT	120
GGTGCCAGCC	TGACCGCCAC	TCTCACATT	GGGCTCTTCG	CTGGCCTTGG	TGGAGCTGGT	180
GCCAGCACCA	GTGGCAGCTC	TGGTGCCTGT	GGTTTCTCCT	ACAAGTGAGA	TTTTAGATAT	240
TGTTAACCT	GCCAGTCTTT	CTCTTCAAGC	CAGGGTGCAT	CCTCAGAAC	CTACTCAACA	300
CAGCACTCTA	GGCAGCCACT	ATCAATCAAT	TGAAGTTGAC	ACTCTGCATT	ARATCTATTT	360
GCCATTCAA	AAAAAAA	AAAA				384

## (2) INFORMATION FOR SEQ ID NO:184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCGAATTGG	GACCGCTGGC	TTATAAGCGA	TCATGTYYNT	CCRGATATKAC	CTCAACGAGC	60
AGGGAGATCG	AGTCTATACG	CTGAAGAAAT	TTGACCCGAT	GGGACAACAG	ACCTGCTCAG	120
CCCATCCTGC	TCGGTTCTCC	CCAGATGACA	AATACTCTSG	ACACCGAATC	ACCATCAAGA	180
AACGCTTCAA	GGTGCTCATG	ACCCAGCAAC	CGCGCCCTGT	CCTCTGAGGG	TCCCTTAAAC	240
TGATGTCTTT	TCTGCCACCT	GTTACCCCTC	GGAGACTCCG	TAACCAAAC	CTTCGGACTG	300
TGAGCCCTGA	TGCCTTTTG	CCAGCCATAC	TCTTGCGAT	CCAGTCTCTC	GTGGCGATTG	360
ATTATGCTTG	TGTGAGGCAA	TCATGGTGGC	ATCACCCATA	AAGGGAACAC	ATTTGACTTT	420
TTTTCTCAT	ATTTAAATT	ACTACMAGAW	TATTWMAGAW	WAAATGAWTT	GAAAAACTST	480
TAAAAAAA	AAAAAA					496

## (2) INFORMATION FOR SEQ ID NO:185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GCTGGTAGCC	TATGGCGKGG	CCCACGGAGG	GGCTCCTGAG	GCCACGGRAC	AGTGAATTCC	60
CAAGTATCYT	GCGCGCGTC	TTCTACCGTC	CCTACCTGCA	GATCTCGGG	CAGATTCCCC	120
AGGAGGACAT	GGACGTGGCC	CTCATGGAGC	ACAGCAACTG	YTCGTCGGAG	CCCGGCTTCT	180
GGGCACACCC	TCCTGGGGCC	CAGGCAGGGCA	CCTGCGTCTC	CCAGTATGCC	AACTGGCTGG	240
TGGTGCTGCT	CCTCGTCATC	TTCTTGCTCG	TGGCCAACAT	CCTGCTGGTC	AACTTGCTCA	300
TTGCCATGTT	CAGTTACACA	TTCGGCAAAG	TACAGGGCAA	CAGCGATCTC	TACTGGGAAG	360

GCGCAGCGTT ACCGCCTCAT CCGG

384

## (2) INFORMATION FOR SEQ ID NO:186:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAGTTAGCTC	CTCCACAAACC	TTGATGAGGT	CGTCTGCAGT	GGCCTCTCGC	TTCATACCGC	60
TNCCATCGTC	ATACTGTAGG	TTGCCACCA	CYTCCCTGGCA	TCTTGGGCG	GCNTAATATT	120
CCAGGAAACT	CTCAATCAAG	TCACCGTCGA	TGAAACCTGT	GGGCTGGTTC	TGTCTTCCGC	180
TCGGTGTGAA	AGGATCTCCC	AGAAGGAGTG	CTCGATCTTC	CCCACACTTT	TGATGACTTT	240
ATTGAGTCGA	TTCTGCATGT	CCAGCAGGAG	GTTGTACCAAG	CTCTCTGACA	GTGAGGTCAC	300
CAGCCCTATC	ATGCCGTTGA	MCGTGCCGAA	GARCACCGAG	CCTTGTGTGG	GGGKKGAAGT	360
CTCACCCAGA	TTCTGCATTA	CCAGAGAGCC	GTGGCAAAAG	ACATTGACAA	ACTCGCCAG	420
GTGGAAAAAAG	AMCAMCTCCT	GGARGTGCTN	GCCGCTCCTC	GTCMGTGTT	GGCAGCGCTW	480
TCCTTTGAC	ACACAAACAA	GTTAAAGGCA	TTTCAGCCC	CCAGAAANTT	GTCATCATCC	540
AAGATNTCGC	ACAGCACTNA	TCCAGTTGGG	ATTAAT			577

## (2) INFORMATION FOR SEQ ID NO:187:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TTGTCTGSTG	AGAATYCATW	60
ACTKGGAAGAA	GMAACATTAA	AGCCTGGACA	CTGGTATTAA	AATTCAACAT	ATGCAACACT	120
TTAAACAGTG	TGTCAATCTG	CTCCCYYNAC	TTTGTCATCA	CCAGTCTGGG	AAKAAGGGTA	180
TGCCCTATTC	ACACCTGTTA	AAAGGGCGCT	AAGCATTGTT	GATTCAACAT	CTTTTTTTTT	240
GACACAAGTC	CGAAAAAAAGC	AAAAGTAAAC	AGTTATYAAAT	TTGTTAGCCA	ATTCACTTTC	300
TTCATGGGAC	AGAGCCATYT	GATTAAAAAA	GCAAATTGCA	TAATATTGAG	CTTYGGGAGC	360
TGATATTGAG	GCGGAAGAGT	AGCCTTTCTA	CTTCACCAGA	CACAACCCC	TTTCATATTG	420
GGATGTTNAC	NAAAGTWATG	TCTCTWACAG	ATGGGATGCT	TTTGTGGCAA	TTCTGTTCTG	480
AGGATCTCCC	AGTTTATTAA	CCACTTGCAC	AAGAAGGCGT	TTTCTTCCTC	AGGC	534

## (2) INFORMATION FOR SEQ ID NO:188:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGAAACCACT	ATCTCTNAAA	ACAACCTCTC	ATACCTTG	GACCTAATT	TGTGTGCGTG	60
TGTGTGTGCG	CGCATATTAT	ATAGACAGGC	ACATCTTTT	TACTTTGTA	AAAGCTTATG	120

CCTCTTGTT	ATCTATATCT	GTGAAAGTTT	TAATGATCTG	CCATAATGTC	TTGGGGACCT	180
TTGTCTTCTG	TGTAAATGGT	ACTAGAGAAA	ACACCTATNT	TATGAGTCAA	TCTAGTTNGT	240
TTTATTCGAC	ATGAAGGAAA	TTTCCAGATN	ACAACACTNA	CAAACCTCTCC	CTKGACKARG	300
GGGGACAAAG	AAAAGCAAAA	CTGAMCATAA	RAAACAAATWA	CCTGGTGAGA	ARTTGATCAA	360
ACAGAAATWR	GGTAGTATAT	TGAARNACAG	CATCATTAAA	RMGTTWTKTT	WTTCCTCC	420
GCAAAAAACA	TGTACNGACT	TCCCCTTGAG	TAATGCCAAG	TTGTTTTTTT	TATNATAAAA	480
CTTGCCCTTC	ATTACATGTT	TNAAAGTGGT	GTGGTGGGCC	AAAATATTGA	AATGATGGAA	540
CTGACTGATA	AAGCTGTACA	AATAAGCAGT	GTGCCTAACAA	AGCAACACAG	TAATGTTGAC	600
ATGCTTAATT	CACAAATGCT	AATTCATTA	TAAATGTTG	CTAAAATACA	CTTGAACTA	660
TTTTCTGTN	TTCCCAGAGC	TGAGATNTTA	GATTTTATGT	AGTATNAAGT	GAAAAANTAC	720
GAAAATAATA	ACATTGAAGA	AAAANANAAA	AAANAAAAAA	A		761

## (2) INFORMATION FOR SEQ ID NO:189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTTTTTTTT	TTGCCGATN	CTACTATTT	ATTGCAGGAN	GTGGGGGTGT	ATGCACCGCA	60
CACCGGGGCT	ATNAGAAGCA	AGAAGGAAGG	AGGGAGGGCA	CAGCCCCTTG	CTGAGCAACA	120
AAGCCGCCTG	CTGCCTTCTC	TGTCTGTCTC	CTGGTGCAGG	CACATGGGA	GACCTTCCCC	180
AAGGCAGGGG	CCACCAGTCC	AGGGTGGGA	ATACAGGGGG	TGGGAGTGT	GCATAAGAAG	240
TGATAGGCAC	AGGCCACCCG	GTACAGACCC	CTCGGCTCCT	GACAGGTNGA	TTTCGACCAG	300
GTCATTGTGC	CCTGCCAGG	CACAGCGTAN	ATCTGGAAAA	GACAGAATGC	TTTCCTTTTC	360
AAATTGGCT	NGTCATNGAA	NGGCANTTT	TCCAANTNG	GCTNGGTCTT	GGTACNCTTG	420
GTCGGGCCA	GCTCCNCGTC	CAAAAANTAT	TCACCCNNCT	CCNAATTGCT	TGCNGGNCCC	480
CC						482

## (2) INFORMATION FOR SEQ ID NO:190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TTTTTTTTT	TTTAAAACA	GTTTTCACA	ACAAAATTAA	TTAGAAGAAT	AGTGGTTTG	60
AAAACCTCTG	CATCCAGTGA	GAACCTACCAT	ACACCACATT	ACAGCTNGGA	ATGTNCTCCA	120
AATGTCTGGT	CAAATGATAC	AATGGAACCA	TTCAATCTTA	CACATGCACG	AAAGAACAAAG	180
CGCTTTGAC	ATACAATGCA	CAAAAAAAA	AGGGGGGGGG	GACCACATGG	ATTAAAATTT	240
TAAGTACTCA	TCACATACAT	TAAGACACAG	TTCTAGTCCA	GTCNAAAATC	AGAACTGCNT	300
TGAAAAATT	CATGTATGCA	ATCCAACCAA	AGAACTTNAT	TGGTGATCAT	GANTNCTCTA	360
CTACATCNAC	CTTGATCATT	GCCAGGAACN	AAAAGTTNAA	ANCACNCNGT	ACAAAAANAA	420
TCTGTAATTN	ANTTCAACCT	CCGTACNGAA	AAATNTNNNT	TATACACTCC	C	471

## (2) INFORMATION FOR SEQ ID NO:191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGATTGA	AGGTCTGTT	TASTGTCGGM	CTGTTCAGCC	ACCAACTCTA	ACAAGTTGCT	60
GTCTTCCACT	CACTGTCTGT	AAGCTTTTA	ACCCAGACWG	TATCTTCATA	AATAGAACAA	120
ATTCTTCACC	AGTCACATCT	TCTAGGACCT	TTTGGATTTC	AGTTAGTATA	AGCTCTTCCA	180
CTTCCTTGT	TAAGACTTCA	TCTGGTAAAG	TCTTAAGTTT	TGTAGAAAGG	AATTYAATTG	240
CTCGTTCTCT	AACAATGTCC	TCTCCTTGAA	GTATTTGGCT	GAACAAACCC	CCTAAAGTCC	300
CTTTGTGCAT	CCATTAA	TATACTTAAT	AGGGCATTGK	TNCACTAGGT	TAAATTCTGC	360
AAGAGTCATC	TGTCTGCAA	AGTTGCGTTA	GTATATCTGC	CA		402

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCTCGGAT	CCAATAATCT	TTGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCYTYTTT	GAYTACCGTG	TGCCAAGTGC	TGGTGATTCT	YAAACACACYT	CCATCCCGYT	180
CTTTGTGGA	AAAACTGGCA	CTTKTCTGGA	ACTAGCARGA	CATCACTTAC	AAATTCAACCC	240
ACGAGACACT	TGAAAGGTGT	AACAAAGCGA	YTCTTGATT	GCTTTTGTC	CCTCCGGCAC	300
CAGTTGTCAA	TACTAACCCG	CTGGTTGCC	TCCATCACAT	TTGTGATCTG	TAGCTCTGGA	360
TACATCTCCT	GACAGTACTG	AAGAACTTCT	TCTTTGTTT	CAAAAGCARC	TCTTGGTGCC	420
TGTTGGATCA	GGTTCCCATT	TCCCAGTCYG	AATGTTACA	TGGCATATT	WACTTCCCAC	480
AAAACATTGC	GATTGAGGC	TCAGCAACAG	CAAATCCTGT	TCCGGCATTG	GCTGCAAGAG	540
CCTCGATGTA	GCCGGCCAGC	GCCAAGGCAG	GCGCCGTGAG	CCCCACCAGC	AGCAGAAGCA	600
G						601

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGCCCC	NATCCCACCA	CGAAGATGCG	CTTGTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCGCTG	TAGCCCCAGC	GAECTCTCAC	CTGCTGGAAG	CGGTTGATGC	TGCACTCYTT	120
CCCAACGCAG	GCAGMAGCGG	GSCCGGTCAA	TGAACCTCAY	TCGTGGCTTG	GGGTKGACGG	180
TKAAGTGCAG	GAAGAGGCTG	ACCACCTCGC	GGTCCACCA	GATGCCCGAC	TGTGCGGGAC	240
CTGCAGCGAA	ACTCCTCGAT	GGTCATGAGC	GGGAAGCGAA	TGAGGCCAG	GGCCTTGCCC	300
AGAACCTTCC	GCCTGTTCTC	TGGCGTCACC	TGCAGCTGCT	GCCGCTGACA	CTCGGCCTCG	360
GACCAGCGGA	CAAACGGCRT	TGAACAGCCG	CACCTCACGG	ATGCCCAAGTG	TGTCGCGCTC	420
CAGGAMMGSC	ACCAGCGTGT	CCAGGTCAAT	GTGGTGAAG	CCCTCCGCGG	GTRATGGCGT	480
CTGCAGTGT	TTTGTGATG	TTCTCCAGGC	ACAGGCTGGC	CAGCTGCGGT	TCATCGAAGA	540
GTCGCGCCTG	CGTGAGCAGC	ATGAAGGCAGT	TGTCGGCTCG	CAGTTCTTCT	TCAGGAACTC	600

CACGCAAT

608

## (2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGGCTGG	ACCTTGCCTC	GCATTGTGCT	TGCTGGCAGG	GAATACCTTG	GCAAGCAGYT	60
CCAGTCCGAG	CAGCCCCAGA	CCGCTGCCGC	CCGAAGCTAA	GCCTGCCTCT	GGCCTTCCCC	120
TCCGCCTCAA	TGCAGAACCA	GTAGTGGGAG	CACTGTGTTT	AGAGTTAAGA	GTGAACACTG	180
TTTGATTTA	CTTGGGAATT	TCCTCTGTTA	TATAGCTTTT	CCCAATGCTA	ATTTCACAAAC	240
AACAACAAACA	AAATAACATG	TTTGCCTGTT	AAGTTGTATA	AAAGTAGGTG	ATTCTGTATT	300
TAAAGAAAAT	ATTACTGTTA	CATAACTGC	TTGCAATTTC	TGTATTTATT	GKTNCTSTGG	360
AAATAAATAT	AGTTATTAAA	GGTTGTCANT	CC			392

## (2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCSTTKGAGG	GGTKAGGKYC	CAGTTYCCGA	GTGGAAGAAA	CAGGCCAGGA	GAAGTGCCTG	60
CCGAGCTGAG	GCAGATGTT	CCACAGTGAC	CCCCAGAGCC	STGGGSTATA	GTYTCTGACC	120
CCTCNCAAGG	AAAGACCACS	TTCTGGGGAC	ATGGGCTGGA	GGGCAGGACC	TAGAGGCACC	180
AAGGGAAGGC	CCCATTCCGG	GGSTGTTCCC	CGAGGAGGAA	GGGAAGGGGC	TCTGTGTGCC	240
CCCCASGAGG	AAGAGGCCCT	GAGTCCTGGG	ATCAGACACC	CCTTCACGTG	TATCCCCACA	300
CAAATGCAAG	CTCACCAAGG	TCCCCTCTCA	GTCCCCCTCC	STACACCCCTG	AMCGGCCACT	360
GSCSCACACC	CACCCAGAGC	ACGCCACCCG	CCATGGGGAR	TGTGCTCAAG	GARTCGCNGG	420
GCARCGTGG	CATCTNGTCC	CAGAAGGGGG	CAGAATCTCC	AATAGANGGA	CTGARCMSTT	480
GCTNANAAAA	AAAAANAAAA	AA				502

## (2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCATT	TTGTCTGCTC	60
CCTCTGGAAG	CCTTGCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATTTT	120
WAGCTGTTK	GAGTTGATTS	GCACCACTGC	ACCCACAACT	TCAATATGAA	AACYAWTTGA	180
ACTWATTTAT	TATCTTGTGA	AAAGTATAAC	AATGAAAATT	TTGTTCATAC	TGTATTKATC	240
AAGTATGATG	AAAAGCAAWA	GATATATATT	CTTTTATTAT	GTTAAATTAT	GATTGCCATT	300

ATTAATCGGC	AAAATGTGGA	GTGTATGTT	TTTCACAGT	AATATATGCC	TTTGTA	360
TCAC	TTGGTT	ATTTATTGT	AAATGARTTA	CAAAATTCTT	AATTAAGAR	420
WATATT	TATT	TCATTAATT	CTTCTKGT	TTACGTWAAT	TTGAAAAGA	480
TCTTGACAGA	AATCGATCTT	GATGCTGTGG	AAGTAGTTG	ACCCACATCC	CTATGAGTT	540
TTCTTAGAAT	GTATAAAGGT	TGTAGCCAT	CNAACTCAA	AGAAAAAAAT	GACCACATAC	600
TTTGCAATCA	GGCTGAAATG	TGGCATGCTN	TTCTAATTCC	AACTTTATAA	ACTAGCAAAN	660
						665

## (2) INFORMATION FOR SEQ ID NO:197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTTTNTTTT	TTTTTTTG	AGGAAGGATT	CCATTATTG	TGGATGCATT	TTCACAATAT	60
ATGTTTATTG	GAGCGATCCA	TTATCAGTGA	AAAGTATCAA	GTGTTATAA	NATTTTAGG	120
AAGGCAGATT	CACAGAACAT	GCTNGTCNGC	TTGCAGTTT	ACCTCGTANA	GATNACAGAG	180
AATTATAGTC	NAACCAGTAA	ACNAGGAATT	TACTTTCAA	AAGATTAAT	CCAAACTGAA	240
CAAAATTCTA	CCCTGAAACT	TACTCCATCC	AAATATTGGA	ATAANAGTCA	GCAGTGATAC	300
ATTCTCTTCT	GAACTTAGA	TTTCTAGAA	AAATATGTAA	TAGTGATCAG	GAAGAGCTCT	360
TGTTCAAAAG	TACAACNAAG	CAATGTTCCC	TTACCATAGG	CCTTAATTCA	AACTTTGATC	420
CATTTCACTC	CCATCACGGG	AGTCAATGCT	ACCTGGGACA	CTTGTATT	GTTCATNCTG	480
ANCNTGGCTT	AA					492

## (2) INFORMATION FOR SEQ ID NO:198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTTNTTTGN	ATTCANTCT	GTANNAANTA	TTTCATTAT	GTTTATTANA	AAAATATNAA	60
TGTNTCCACN	ACAAATCATN	TTACNTNAGT	AAGAGGCCAN	CTACATTGTA	CAACATACAC	120
TGAGTATATT	TTGAAAAGGA	CAAGTTAAA	GTANACNCAT	ATTGCCGANC	ATANCACATT	180
TATACATGGC	TTGATTGATA	TTTAGCACAG	CANAAACTGA	GTGAGTTACC	AGAAAANAAAT	240
NATATATGTC	AATCNGATT	AAGATACAAA	ACAGATCCTA	TGGTACATAN	CATCNTGTAG	300
GAGTTGTGGC	TTTATGTTA	CTGAAAGTCA	ATGCAGTTCC	TGTACAAAGA	GATGGCCGTA	360
AGCATTCTAG	TACCTCTACT	CCATGGTTAA	GAATCGTACA	CTTATGTTA	CATATGTNCA	420
GGGTAAGAAT	TGTGTTAAGT	NAANTTATGG	AGAGGTCCAN	GAGAAAAATT	TGATNCAA	478

## (2) INFORMATION FOR SEQ ID NO:199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

AGTGACTTGT	CCTCCAACAA	AACCCTTGA	TCAAGTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCCTG	CAAATCTATT	CCTACTTGT	CGGACTTTGA	180
AGTGATTCA	TTTCCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGCTTTA	240
TGAAGCCNAC	TCTGAACACG	CTGGTTATCT	NAGATGAGAA	NCAGAGAAAT	AAAGTCNAGA	300
AAATTACCT	GGANGAAAAG	AGGCTTNGG	CTGGGGACCA	TCCCATTGAA	CCTTCTCTTA	360
ANGGACTTTA	AGAANAAAAT	ACCACATGTN	TGTNGTATCC	TGGTGCCNGG	CCGTTTANTG	420
AACNTNGACN	NCACCCTNT	GGAATANANT	CTTGACNGCN	TCCTGAACTT	GCTCCTCTGC	480
GA						482

## (2) INFORMATION FOR SEQ ID NO:200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CGGCCGCAAG	TGCAACTCCA	GCTGGGGCCG	TGCGGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTGCGAC	GACGGCGGCG	GCGACAGTCG	CAGGTGCAGC	GCAGGGCGCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCCGCA	GAGGTCGTGT	CACGTCCCAC	GACCTTGACG	CCGTCGGGGA	180
CAGCCGGAAC	AGAGCCCGGT	GAANGCGGG	GGCCTCGGGG	AGCCCCTCGG	GAAGGGCGGC	240
CCGAGAGATA	CGCAGGTGCA	GGTGGCCGCC				270

## (2) INFORMATION FOR SEQ ID NO:201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTTTTTTTT	TTTTGGAATC	TACTGCGAGC	ACAGCAGGTC	AGCAACAAAGT	TTATTTGCA	60
GCTAGCAAGG	TAACAGGGTA	GGGCATGGTT	ACATGTTAG	GTCAACTTCC	TTTGTCTGG	120
TTGATTGGTT	TGTCTTATG	GGGGCGGGGT	GGGGTAGGGG	AAANCGAAGC	ANAANTAAACA	180
TGGAGTGGGT	GCACCCTCCC	TGTAGAACCT	GGTTACNAAA	GCTTGGGGCA	GTTCACCTGG	240
TCTGTGACCG	TCATTTCTT	GACATCAATG	TTATTAGAAG	TCAGGATATC	TTTTAGAGAG	300
TCCACTGTNT	CTGGAGGGAG	ATTAGGGTTT	CTTGCCAANA	TCCAANAAA	ATCCACNTGA	360
AAAAGTTGGA	TGATNCANGT	ACNGAATAACC	GANGGCATAN	TTCTCATANT	CGGTGGCCA	419

## (2) INFORMATION FOR SEQ ID NO:202:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTNTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	60
TGGCACTTAA	TCCATTAA	TTTCAAAATG	TCTACAAANT	TTNAATNCNC	CATTATAACNG		120
GTNATTTCNC	AAAATCTAAA	NNNTTATTCAA	ATNTNAGCCA	AANTCCTTAC	NCAAATNNAA		180
TACNCNCAAA	AATCAAAAAT	ATACNTNTCT	TTCAGCAAAC	TTNGTTACAT	AAATTAAAAA		240
AATATATACG	GCTGGTGT	TCAAAGTACA	ATTATCTTAA	CACTGCAAAC	ATNTTTNNAA		300
GGAACTAAAAA	TAAAAA	CACTNCCGCA	AAGGTTAAAG	GGAAACAACAA	ATTCTNTTTA		360
CAACANCNNC	NATTATAAAA	ATCATATCTC	AAATCTTAGG	GGAAATATATA	CTTCACACNG		420
GGATCTTAAC	TTTTACTNCA	CTTTGTTTAT	TTTTTANAA	CCATTGTNTT	GGGCCCAACAA		480
CAATGGNAAT	NCCNCNCNC	TGGACTAGT					509

## (2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TTTTTTTTT	TTTTTTTG	CCCCCTCTT	ATAAAAACA	AGTTACCATT	TTATTTACT	60
TACACATATT	TATTTATAA	TTGGTATTAG	ATATTCAAA	GGCAGCTTT	AAAATCAAAC	120
TAAATGGAAA	CTGCCTAGA	TACATAATT	TTAGGAATTA	GCTAAAATC	TGCCTAAAGT	180
GAAAATCTTC	TCTAGCTCTT	TTGACTGTAA	ATTTTGACT	CTTGTAAAAC	ATCCAAATT	240
ATTTTCTTG	TCTTAAAAT	TATCTAATCT	TTCCATT	TCCCTATTCC	AAGTCAATT	300
GCTTCTCTAG	CCTCATTCC	AGCTCTTAT	CTACTATTAG	TAAGTGGCTT	TTTCCTAAA	360
AGGGAAAACA	GGAAGAGANA	ATGGCACACA	AAACAAACAT	TTTATATTCA	TATTTCTACC	420
TACGTTAATA	AAATAGCATT	TTGTGAAGCC	AGCTAAAAG	AAGGCTTAGA	TCCTTTATG	480
TCCATTTAG	TCACTAAACG	ATATCNAAG	TGCCAGAATG	CAAAGGTTT	GTGAACATT	540
ATTCAAAAGC	TAATATAAGA	TATTCACAT	ACTCATCTT	CTG		583

## (2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTTTTTTTNT	TTTTTTNCTC	TTCTTTTTT	TTGANAATGA	GGATCGAGTT	60
TTTCACTCTC	TAGATAGGGC	ATGAAGAAAA	CTCATCTTTC	CAGCTTAAA	120
AATCTCTTAT	GCTATATCAT	ATTTTAAGTT	AAACTAATGA	GTCACTGGCT	180
TGAAGGAAAT	CTGTCATTC	TTCTCATTCA	TATAGTTATA	TCAAGTACTA	240
TGAGAGGTTT	TTCTCTCTA	TTTACACATA	TATTCACATG	TGAATTGTA	300
ATTTTCATGC	AAACTAGAAA	ATAATGTNTT	CTTTGCATA	AGAGAAGAGA	360
CATTACAAAA	CTGCTCAAAT	TGTTGTTAA	GNTTATCCAT	TATAATTAGT	420
CTAATACAAA	TCACATTAC	NGACNAGCAA	TAATAAAACT	GAAGTACCAAG	480
AAAATAATTA	AAGGAACATT	TTTAGCCTGG	GTATAATTAG	CTAATTCACT	540
TTATTNAGAA	TGAATTACA	TGTTATTATT	CCNTAGCCCA	ACACAATGG	589

## (2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TTTTNTTTT	TTTTTCAGT	AATAATCAGA	ACAATATTAA	TTTTTATATT	TAAAATTCA	60
AGAAAAGTGC	CTTACATTAA	ATAAAAGTTT	GTTCCTCAAA	GTGATCAGAG	GAATTAGATA	120
TNGTCTTGAA	CACCAATATT	AATTGAGGA	AAATACACCA	AAATACATTAA	AGTAAATTAT	180
TTAAGATCAT	AGAGCTTGTA	AGTAAAAGA	TAAAATTGA	CCTCAGAAAC	TCTGAGCATT	240
AAAAATCCAC	TATTAGCAAA	TAAATTACTA	TGGACTTCTT	GCTTTAATT	TGTGATGAAT	300
ATGGGGTGTGTC	ACTGGTAAAC	CAACACATT	TGAAGGATAC	ATTACTTAGT	GATAGATTCT	360
TATGTACTTT	GCTANATNAC	GTGGATATGA	GTTGACAAGT	TTCTCTTCT	TCAATCTTT	420
AAGGGCNGA	NGAAATGAGG	AAGAAAAGAA	AAGGATTACG	CATACTGTT	TTTCTATNGG	480
AAGGATTAGA	TATGTTCC	TTGCCAATAT	TAAAAAAATA	ATAATGTTA	CTACTAGTGA	540
					AACCC	545

## (2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 487 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TTTTTTTTT	TTTTTAGTC	AAGTTCTNA	TTTTTATTAT	AATTAAAGTC	TTGGTCATT	60
CATTATTAG	CTCTGCAACT	TACATATTAA	AATTAAAGAA	ACGTTNTTAG	ACAACGTNA	120
CAATTATAA	ATGTAAGGTG	CCATTATTGA	GTANATATAT	TCCTCCAAGA	GTGGATGTGT	180
CCCTTCTCCC	ACCAACTAAT	GAANCAGCAA	CATTAGTTA	ATTTTATTAG	TAGATNATAC	240
ACTGCTGCAA	ACGCTAATT	TCTCTCCAT	CCCCATGTNG	ATATTGTGA	TATGTGTGAG	300
TTGGTNAGAA	TGCATCANCA	ATCTNACAAT	CAACAGCAAG	ATGAAGCTAG	GCNTGGGCTT	360
TCGGTGAAA	TAGACTGTGT	CTGTCTGAAT	CAAATGATCT	GACCTATCCT	CGGTGGCAAG	420
AACTCTTCGA	ACCGCTTCCT	CAAAGGCNGC	TGCCACATT	GTGGCNTCTN	TTGCACTTGT	480
					TTCAAAA	487

## (2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 332 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TGAATTGGCT	AAAAGACTGC	ATTTTTANAA	CTAGCAACTC	TTATTTCTTT	CCTTTAAAAAA	60
TACATAGCAT	TAAATCCCAA	ATCCTATTAA	AAGACCTGAC	AGCTTGAGAA	GGTCACTACT	120
GCATTTATAG	GACCTTCTGG	TGGTTCTGCT	GTTACNTTTG	AANTCTGACA	ATCCTTGANA	180
ATCTTGACAT	GCAGAGGAGG	TAAAAGGTAT	TGGATTTCA	CAGAGGAANA	ACACAGCGCA	240
GAAATGAAGG	GGCCAGGCTT	ACTGAGCTG	TCCACTGGAG	GGCTCATGGG	TGGGACATGG	300

AAAAGAAGGC AGCCTAGGCC CTGGGGAGCC CA

332

## (2) INFORMATION FOR SEQ ID NO:208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGGGCGTGGT	GC GGAGGGCG	TTACTGTTT	GTCTCAGTAA	CAATAAATAC	AAAAAGACTG	60
GTTGTGTTCC	GGCCCCATCC	AACCACGAAG	TTGATTCTC	TTGTGTGCAG	AGTGACTGAT	120
TTTAAAGGAC	ATGGAGCTTG	TCACAATGTC	ACAATGTCAC	AGTGTGAAGG	GCACACTCAC	180
TCCC CGTGA	TTCACATT	GCAACCAACA	ATAGCTCATG	AGTCCATACT	TGTAAATACT	240
TTTGGCAGAA	TACTTNTTGA	AACTTGCAGA	TGATAACTAA	GATCCAAGAT	ATTTC CCAAA	300
GTAAATAGAA	GTGGGTCTATA	ATATTAATTA	CCTGTTACA	TCAGCTTCCA	TTTACAAGTC	360
ATGAGCCCAG	ACACTGACAT	CAAACTAAGC	CCACTTAGAC	TCCTCACCAC	CAGTCTGTCC	420
TGTCATCAGA	CAGGAGGCTG	TCACCTTGAC	CAAATTCTCA	CCAGTCAATC	ATCTATCCAA	480
AAACCATTAC	CTGATCCACT	TCCGGTAATG	CACCACCTTG	GTGA		524

## (2) INFORMATION FOR SEQ ID NO:209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGTGAGGAA	ATCCAGAGTT	GCCATGGAGA	AAATTCCAGT	GTCAGCATT	TTGCTCCTTG	60
TGGCCCTCTC	CTACACTCTG	GCCAGAGATA	CCACAGTCAA	ACCTGGAGCC	AAAAAGGACA	120
CAAAGGACTC	TCGACCCAAA	CTGCCCCAGA	CCCTCTCCA			159

## (2) INFORMATION FOR SEQ ID NO:210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

ACTCCCTGGC	AGACAAAGGC	AGAGGAGAGA	GCTCTGTTAG	TTCTGTGTTG	TTGAAGTGC	60
ACTGAATTTC	TTTCCACTTG	GACTATTACA	TGCCANTG	GGGACTAATG	AAAAAACGTA	120
TGGGGAGATT	TTANCCAATT	TANGTNTGTA	AATGGGGAGA	CTGGGGCAGG	CGGGAGAGAT	180
TTGCAGGGTG	NAAATGGGAN	GGCTGGTTG	TTANATGAAC	AGGGACATAG	GAGGTAGGCA	240
CCAGGATGCT	AAATCA					256

## (2) INFORMATION FOR SEQ ID NO:211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ACATTGTTT	TTTGAGATAA	AGCATTGAGA	GAGCTCTCCT	TAACGTGACA	CAATGGAAGG	60
ACTGGAACAC	ATACCCACAT	CTTTGTTCTG	AGGGATAATT	TTCTGATAAA	GTCTTGCTGT	120
ATATTCAAGC	ACATATGTTA	TATATTATTTC	AGTTCCATGT	TTATAGCCTA	GTAAAGGAGA	180
GGGGAGATAC	ATTNGAAAG	AGGACTGAAA	GAAATACTCA	AGTNGGAAA	CAGAAAAAGA	240
AAAAAAGGAG	CAAATGAGAA	GCCT				264

## (2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ACCCAAAAAT	CCAATGCTGA	ATATTGGCT	TCATTATTCC	CANATTCTT	GATTGTCAAA	60
GGATTTAATG	TTGTCTCAGC	TTGGGCACCT	CAGTTAGGAC	CTAAGGATGC	CAGCCGGCAG	120
GTTTATATAT	GCAGCAACAA	TATTCAAGCG	CGACAACAGG	TTATTGAACT	TGCCCGCCAG	180
TTNAATTCA	TTCCCATTGA	CTTGGGATCC	TTATCATCAG	CCAGAGAGAT	TGAAAATTAA	240
CCCCTACNAC	TCTTTACTCT	CTGGANAGGG	CCAGTGGTGG	TAGCTATAAG	CTTGGCCACA	300
TTTTTTTTTC	CTTTATTCCCT	TTGTCAGA				328

## (2) INFORMATION FOR SEQ ID NO:213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACTTATGAGC	AGAGCGACAT	ATCCNAGTGT	AGACTGAATA	AAACTGAATT	CTCTCCAGTT	60
TAAAGCATTG	CTCACTGAAG	GGATAGAAGT	GACTGCCAGG	AGGGAAAGTA	AGCCAAGGCT	120
CATTATGCCA	AAGGANATAT	ACATTTCAAT	TCTCCAAACT	TCTTCCTCAT	TCCAAGAGTT	180
TTCAATATTT	GCATGAACCT	GCTGATAANC	CATGTTAANA	AACAAATATC	TCTCTNACCT	240
TCTCATCGGT						250

## (2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ACCCAGAATC	CAATGCTGAA	TATTTGGCTT	CATTATTCCC	AGATTCTTG	ATTGTCAAAG	60
GATTTAATGT	TGTCTCAGCT	TGGGCACTTC	AGTTAGGACC	TAAGGATGCC	AGCCGGCAGG	120
TTTATATATG	CAGCAACAAT	ATTCAAGCGC	GACAACAGGT	TATTGAACCT	GCCCGCCAGT	180
TGAATTTCAT	TCCCATTGAC	TTGGGATCCT	TATCATCAGC	CANAGAGATT	GAAAATTAC	240
CCCTACGACT	CTTTACTCTC	TGGAGAGGGC	CAGTGGTGGT	AGCTATAAGC	TTGGCCACAT	300
TTTTTTTCC	TTTATTCCCT	TGTCAGAGAT	GCGATTCATC	CATATGCTAN	AAACCAACAG	360
AGTGACTTTT	ACAAAATTCC	TATAGANATT	GTGAATAAAA	CCTTACCTAT	AGTTGCCATT	420
ACTTGCTCT	CCCTAATATA	CCTC				444

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 366 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ACTTATGAGC	AGAGCGACAT	ATCCAAGTGT	ANACTGAATA	AAACTGAATT	CTCTCCAGTT	60
TAAAGCATTG	CTCACTGAAG	GGATAGAAGT	GAUTGCCAGG	AGGGAAAGTA	AGCCAAGGCT	120
CATTATGCCA	AAGGANATAT	ACATTCAAT	TCTCCAAACT	TCTTCCTCAT	TCCAAGAGTT	180
TTCAATATTT	GCATGAACCT	GCTGATAAGC	CATGTTGAGA	AACAAATATC	TCTCTGACCT	240
TCTCATCGGT	AAGCAGAGGC	TGTAGGCAAC	ATGGACCATA	GCGAANAAAA	AACTTAGTAA	300
TCCAAGCTGT	TTTCTACACT	GTAACCAGGT	TTCCAACCAA	GGTGGAAATC	TCCTATACTT	360
					GGTGCC	366

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 260 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGTATAAAC	AGAACTCCAC	TGCANGAGGG	AGGGCCGGGC	CAGGAGAAC	TCCGCTTGTC	60
CAAGACAGGG	GCCTAAGGAG	GGTCTCCACA	CTGCTNNNTAA	GGGCTNTTNC	ATTTTTTTAT	120
TAATAAAAAG	TNNAAAAGGC	CTCTTCTCAA	CTTTTTCCC	TTNGGCTGGA	AAATTTAAAA	180
ATCAAAAATT	TCCTNAAGTT	NTCAAGCTAT	CATATATACT	NTATCCTGAA	AAAGCAACAT	240
					AATTCTTCCTT	260

(2) INFORMATION FOR SEQ ID NO:217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG GTAAGTTAN AAATGTTATA ATTCAGGAA NAGGAACGCA TATAATTGTA	60
TCTTGCTAT AATTTCTAT TTTAATAAGG AAATAGCAAA TTGGGGTGGG GGGAAATGTAG	120
GGCATTCTAC AGTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAATTTC	180
ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATTG ATAATTAGCC ACTTACCCCTA	240
ATATCCTTCA TGCTTGTAAA GT	262

## (2) INFORMATION FOR SEQ ID NO:218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCCAA CCCCTGAGCA	60
CCCCTATCAA CTCCCTTTG TAGTAAACTT GGAACCTTGG AAATGACCAG GCCAAGACTC	120
AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGTNTNA NGTCCAGGGT TGCTAGGAAA	180
ANAAATCAGC AGACACAGGT GTAAA	205

## (2) INFORMATION FOR SEQ ID NO:219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTG TCTCAGTAAC AATAAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA	60
ACCACGAAGT TGATTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA	114

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

ACTAGCCAGC ACAAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTAC ATTTCTTTA	60
AAATAAGCAT TTAGTGCTCA GTCCCTACTG AGT	93

## (2) INFORMATION FOR SEQ ID NO:221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ACTANGTGCA GGTGCGCACA AATATTTGTC GATATTCCCT TCATCTTGA TTCCATGAGG	60
TCTTTGCCC AGCCTGTGGC TCTACTGTAG TAAGTTCTG CTGATGAGGA GCCAGNATGC	120
CCCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT	167

## (2) INFORMATION FOR SEQ ID NO:222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCCC	60
GTTCTTCACC TGTCCCCCAA TCCTTAAAAG GCCATACTGC ATAAAGTCAA CAACAGATAA	120
ATGTTTGCTG AATTAAAGGA TGGATGAAAA AAATTAATAA TGAATTTTTG CATAATCCAA	180
TTTTCTCTTT TATATTCTA GAAGAAGTTT CTTGAGCCT ATTAGATCCC GGAATCTTT	240
TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCTTTACA TATATCTGGC ATATTGAGT	300
CTCGTATCAA AACAAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T	351

## (2) INFORMATION FOR SEQ ID NO:223

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACAAACA AACAAAAAAA ACAATTCTTC ATTCAAGAAA ATTATCTTAG GGACTGATAT	60
TGGTAATTAT GGTCAATTAA ATWRTRTTKT GGGGCATTTC CTTACATTGT CTTGACAAGA	120
TTAAAATGTC TGTGCCAAAA TTTTGTATT TATTGGAGA CTTCTTATCA AAAGTAATGC	180
TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTGGAG TGTGCTATT	240
TAAAAGATT TGATTTCCTG GAATGACAAT TATATTAA CTTTGGTGGG GGAAANAGTT	300
ATAGGACCAC AGTCTTCACT TCTGATACTT GTAAATTAAT CTTTATTGC ACTTGTGTTG	360
ACCATTAAGC TATATGTTA AAA	383

## (2) INFORMATION FOR SEQ ID NO:224

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

CCCCTGAAGG	CTTCTTGT	TA GAAAATAGTA	CAGTTACAAC	CAATAGGAAC	AACAAAAAGA	60
AAAAGTTGT	GACATTGT	AG TAGGGAGTGT	GTACCCCTTA	CTCCCCATCA	AAAAAAAAT	120
GGATACATGG	TTAAAGGATA	RAAGGGCAAT	ATTTTATCAT	ATGTTCTAAA	AGAGAAGGAA	180
GAGAAAATAC	TACTTCTCR	AAATGGAAGC	CCTTAAAGGT	GCTTGATAC	TGAAGGACAC	240
AAATGTGGCC	GTCCATCCTC	CTTTARAGTT	GCATGACTTG	GACACGGTAA	CTGTTGCAGT	300
TTTARACTCM	GCATTGTGAC					320

EQUITY INVESTMENT FUNDING INC.

## CLAIMS

1. A method for detecting prostate cancer in a patient, comprising:

- contacting a biological sample obtained from the patient with a binding agent which is capable of binding to a polypeptide, the polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and
- detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting prostate cancer in the patient.

2. The method of claim 1 wherein the binding agent is a monoclonal antibody.

3. The method of claim 2 wherein the binding agent is a polyclonal antibody.

4. A method for monitoring the progression of prostate cancer in a patient, comprising:

- contacting a biological sample obtained from the patient with a binding agent that is capable of binding to a polypeptide, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences;
- determining in the sample an amount of a protein or polypeptide that binds to the binding agent;
- repeating steps (a) and (b); and

(d) comparing the amount of polypeptide detected in steps (b) and (c) to monitor the progression of prostate cancer in the patient.

5. A monoclonal antibody that binds to a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 8-29, 41-45, 47-52, 54-65, 70, 73, 74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

6. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient a therapeutically effective amount of a monoclonal antibody according to claim 5.

7. The method of claim 6 wherein the monoclonal antibody is conjugated to a therapeutic agent.

8. A method for detecting prostate cancer in a patient comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotides is specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting prostate cancer.

9. The method of claim 8, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a

sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

10. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies of claim 5; and
- (b) a detection reagent.

11. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies that bind to a polypeptide encoded by a DNA molecule having a nucleotide sequence selected from the group consisting of SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, the complements of said sequences and variants of said nucleotide sequences; and
- (b) a detection reagent.

12. The kit of claims 10 or 11 wherein the monoclonal antibodies are immobilized on a solid support.

13. The kit of claim 12 wherein the solid support comprises nitrocellulose, latex or a plastic material.

14. The kit of claims 10 or 11 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

15. The kit of claim 14 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.

16. The kit of claim 14 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

17. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule encoding a

polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.

18. A diagnostic kit of claim 17 wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

19. A method for detecting prostate cancer in a patient, comprising:  
(a) obtaining a biological sample from the patient;  
(b) contacting the biological sample with an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and  
(c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting prostate cancer in the patient.

20. The method of claim 19 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

21. A diagnostic kit comprising an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences

recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

22. The diagnostic kit of claim 21 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

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COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER  
AND METHODS FOR THEIR USE

ABSTRACT OF THE DISCLOSURE

Compounds and methods for diagnosing prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for preparing probes, primers, and polypeptides are also provided.

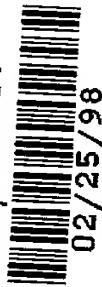
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PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Jiangchun Xu and Davin C. Dillon  
Filed : February 25, 1998  
For : COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE  
CANCER AND METHODS FOR THEIR USE  
Docket No. : 210121.428C3  
Date : February 25, 1998

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09/030606  
02/25/98



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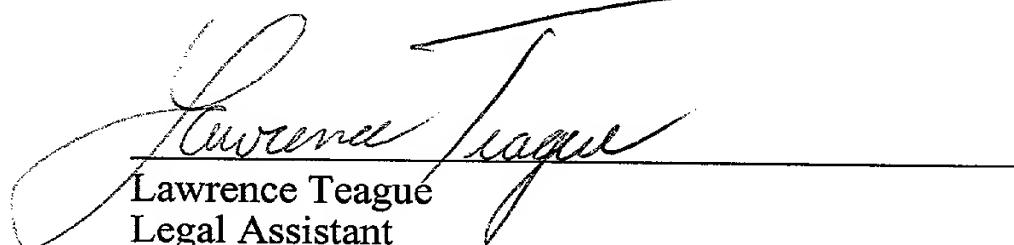
DECLARATION

Sir:

I, Lawrence Teague, in accordance with 37 C.F.R. § 1.821(f) do hereby declare that, to the best of my knowledge, the content of the paper entitled "Sequence Listing" and the computer readable copy contained within the floppy disk are the same.

I declare further that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true and further that these statements are made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Dated this 25th day of February, 1998.



Lawrence Teague  
Legal Assistant

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